

*****STN, Columbus*****

FILE 'HOME' ENTERED AT 11:17:29 ON 13 OCT 2003

=> file biosis,caba,caplus,embase,japio,lifesci,medline,scisearch,uspatfull

=> e trucksis michele/au

E1 1 TRUCKSIS F E/AU
E2 114 TRUCKSIS M/AU
E3 36 --> TRUCKSIS MICHELE/AU
E4 1 TRUCL NIKA/AU
E5 1 TRUCLOCK ELBERT P/AU
E6 1 TRUCO E/AU
E7 1 TRUCO L B/AU
E8 1 TRUCO LOUIS/AU
E9 1 TRUCO LUIZ C/AU
E10 37 TRUCO M J/AU
E11 2 TRUCO MARIA J/AU
E12 2 TRUCO MARIA JOSE/AU

=> s e2-e3 and mycobacter?

L1 46 ("TRUCKSIS M"/AU OR "TRUCKSIS MICHELE"/AU) AND MYCOBACTER?

=> dup rem l1

PROCESSING COMPLETED FOR L1

L2 18 DUP REM L1 (28 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 18 ANSWERS - CONTINUE? Y/(N):y

L2 ANSWER 1 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2003:23515 BIOSIS

DN PREV200300023515

TI The goldfish model of ***Mycobacterium*** marinum pathogenesis:

Applications to tuberculosis vaccine development.

AU ***Trucksis, Michele***

SO Tuberculosis (Edinburgh), (2002) Vol. 82, No. 2-3, pp. 141. print.

Meeting Info.: International Symposium on Current Developments in Drug

Discovery for Tuberculosis Bangalore, India January 14-17, 2002

ISSN: 1472-9792.

DT Conference

LA English

L2 ANSWER 2 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:584921 BIOSIS

DN PREV200200584921

TI Initial characterization of an araC homologue in ***Mycobacterium***
marinum.

AU Pritchett, C. L. (1); ***Trucksis, M. (1)***

CS (1) University of Maryland, Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology,

(2002) Vol. 102, pp. 75-76. <http://www.asmta.org/mtgsrc/generalmeeting.htm>

m. print.

Meeting Info.: 102nd General Meeting of the American Society for

Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for

Microbiology

. ISSN: 1060-2011.

DT Conference

LA English

AB ***Mycobacterium*** tuberculosis, the etiologic agent of tuberculosis,
continues to kill approximately 3 million people every year. Our
laboratory has chosen to study a close relative of M. tuberculosis, M.
marinum, in an effort to understand ***mycobacterial*** pathogenesis.
Signature-tagged mutagenesis of M. marinum in concert with the goldfish
model of ***mycobacterial*** pathogenesis identified thirty-six
unique, potential virulence mutants. One mutant identified contained an
insertion in an araC homologue. Complete sequence of the gene was
obtained. A search against the M. tuberculosis genome identified a 73%

identical gene homologue. AraC homologues have been found to regulate virulence factors, stress responses, and metabolic pathways. To understand the regulation of the araC homologue, we determined the promoter region of the araC homologue by cloning the araC homologue with upstream flanking sequence into a promoterless xylE reporter vector creating transcriptional fusions. xylE encodes catechol 2,3 dioxygenase, an enzyme that cleaves catechol producing a spectrophotometrically detectable product. A genomic fragment 2.2 kb upstream of the predicted araC translational start site had XylE activity of 1102±498 mU/mg compared to the vector alone which had activity of 45.5±50.5 mU/mg ($p<0.002$). Smaller genomic upstream fragments of 1.1 and 0.5 kb showed no significant XylE activity. Together the fusion data suggested the presence of a promoter between 1.1 and 2.2 kb upstream of the araC homologue. Computer analysis of the predicted upstream region of the araC homologue identified no consensus sequences with known *E. coli* promoters, but did identify several possible

mycobacterial promoters based on homology to previously identified ***mycobacterial*** promoters. In conclusion, we have identified a promoter upstream of the araC homologue that may control the expression of the araC homologue, a putative virulence factor. Further experiments are underway to confirm the promoter region, identify optimal conditions for expression, and determine the role of the araC homologue as it pertains to virulence.

L2 ANSWER 3 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:570980 BIOSIS

DN PREV200200570980

TI Identification of a cutinase gene in ***Mycobacterium*** marinum linked to virulence.

AU Ruley, K. M. (1); ***Trucksis, M. (1)***

CS (1) University of Maryland, Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 58. <http://www.asmsa.org/mtgsrc/generalmeeting.htm>. print.

Meeting Info.: 102nd General Meeting of the American Society for Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for Microbiology

. ISSN: 1060-2011.

DT Conference

LA English

AB ***Mycobacterium*** tuberculosis, the causative agent of tuberculosis, infects one-third of the world's population and kills 3 million persons annually. Our laboratory has developed a surrogate model for ***mycobacterial*** pathogenesis, using *Mycobacterium marinum* and the goldfish. We have applied signature-tagged mutagenesis (STM) to our model, and identified 36 unique virulence mutants. One mutant (*M. marinum* 62.6) identified twice in the STM screen, has the transposon inserted in a gene with homology to a *M. tuberculosis* cutinase gene. Competition assay studies show that *M. marinum* 62.6 is out-competed by the wild type strain (ATCC 927), with a competitive index of 0.29, further corroborating the mutant's attenuation in vivo. Cutinases are secreted enzymes in the esterase family found in pathogenic fungi and bacteria that degrade cutin, an insoluble polysaccharide commonly found on the waxy surface of plants. As secreted enzymes, cutinase activity can be detected using an agarose gel overlay supplemented with the substrate p-nitrophenol butyrate (PNB), which when hydrolyzed, turns from colorless to bright yellow. A PNB overlay of wild-type *M. marinum* and 62.6 displayed cutinase activity, however a search of the *M. tuberculosis* genome identified 5 cutinase gene homologues, suggesting that other cutinase genes are responsible for the cutinase activity seen in the assay of *M. marinum* 62.6. *E. coli* strain VCS257 did not exhibit cutinase activity. When the *M. marinum* cutinase gene was cloned into *E. coli* VCS257, cutinase activity was evident.

However, when the cutinase gene of *M. marinum* was interrupted by the IS 1096 transposon, and cloned into *E. coli* VCS257, the cutinase activity was abolished. Therefore, the gene interrupted by the transposon is responsible for cutinase activity. In conclusion, we have identified a *M. marinum* mutant that is defective in cutinase activity and is attenuated in virulence in vivo by STM and competition assay. Additional experiments are in progress to complement the cutinase gene in vivo to restore virulence.

L2 ANSWER 4 OF 18 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN DUPLICATE 1

AN 2002425675 EMBASE

TI Goldfish as an animal model system for ***mycobacterial*** infection.

AU Ruley K.M.; Reimschuessel R.; ***Trucksis M.***

CS K.M. Ruley, Center for Vaccine Development, Univ. of Maryland School of Medicine, Baltimore, MD 21201, United States

SO Methods in Enzymology, (2002) 358/- (29-39).

Refs: 16

ISSN: 0076-6879 CODEN: MENZAU

CY United States

DT Journal; Article

FS 004 Microbiology

005 General Pathology and Pathological Anatomy

015 Chest Diseases, Thoracic Surgery and Tuberculosis

LA English

L2 ANSWER 5 OF 18 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2001:208420 CAPLUS

DN 134:247979

TI Virulence genes of ***Mycobacterium*** marinum and *M. tuberculosis*, avirulent mutant ***mycobacteria*** and attenuated vaccines

IN ***Trucksis, Michele***

PA University of Maryland, Baltimore, USA; United States Government, as Represented by Department of Veterans Affairs

SO PCT Int. Appl., 99 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001019993	A2	20010322	WO 2000-US25512	20000918
WO 2001019993	A3	20011122		

PI WO 2001019993 A2 20010322 WO 2000-US25512 20000918

WO 2001019993 A3 20011122

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-154322P P 19990917

AB Methods for identifying, isolating and mutagenizing virulence genes of ***mycobacteria***, e.g., ***Mycobacterium*** marinum and *M. tuberculosis*, are described. The *M. marinum* signature-tagged mutant library was generated and screened for mutants which exhibit a reduced ability to survive in the goldfish model. Wild type *M. marinum* virulence genes which correspond to the genes disrupted by transposon in avirulent mutants were isolated. *M. tuberculosis* genes homologous to *M. marinum* virulence genes were isolated and characterized. Also described are isolated virulence genes and fragments of them, isolated gene products and

fragments of them, avirulent bacteria in which one or more virulence genes are mutagenized, attenuated vaccines contg. such mutant bacteria, and methods to elicit an immune response in a host, using such mutant bacteria.

L2 ANSWER 6 OF 18 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2000:853027 SCISEARCH

GA The Genuine Article (R) Number: 371LP

TI Fishing for ***mycobacterial*** virulence genes: a promising animal model

AU ***Trucksis M***

CS UNIV MARYLAND, SCH MED, DEPT MED, CTR VACCINE DEV, BALTIMORE, MD 21201

CYA USA

SO ASM NEWS, (NOV 2000) Vol. 66, No. 11, pp. 668-674.

Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904.

ISSN: 0044-7897.

DT Article; Journal

LA English

REC Reference Count: 9

L2 ANSWER 7 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

DUPLICATE 2

AN 2000:118645 BIOSIS

DN PREV200000118645

TI Transformation and transposition of the genome of ***Mycobacterium*** marinum.

AU Talaat, Adel M. (1); ***Trucksis, Michele***

CS (1) University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd, Dallas, TX, 75235 USA

SO American Journal of Veterinary Research, (Feb., 2000) Vol. 61, No. 2, pp. 125-128.

ISSN: 0002-9645.

DT Article

LA English

SL English

AB Objective: To develop and evaluate protocols for genetic manipulations (transformation and transposition) of the fish pathogen, ***Mycobacterium*** marinum. Sample Population: Isolates of M marinum obtained from fish and humans. Procedure: Electrocompetent cells were prepared from isolates of M marinum grown to various growth phases at several temperatures and with or without the addition of ethionamide or cycloheximide. ***Mycobacterial*** cells were transformed by electroporation with a replicative Escherichia coli- ***mycobacteria*** shuttle vector (pYUB18) as well as suicide vectors (pYUB285 and pUS252) that carried transposable elements (IS 1096 and IS 6110, respectively). Mutants from both isolates of M marinum were recovered on 7H10 agar plates supplemented with kanamycin. Transformation and transposition efficiencies for various protocols were compared. Southern hybridization analysis was performed on ***mycobacterial*** mutants to confirm transposition events. Results: Competent cells prepared at room temperature (23-25 C) from organisms in late-exponential growth phase yielded higher transposition efficiency, compared with cells prepared at 4 C or from organisms in early- or mid-exponential growth phase. Naturally developing kanamycin-resistant colonies of M marinum were not detected. Only the IS 1096-derived transposition was able to efficiently mutate M marinum. Southern hybridization of M marinum mutants revealed random integration of IS 1096 into the M marinum genome. Conclusions: Transposition and transformation efficiencies were comparable, suggesting that the limiting factor in transposition is the transformation step. Most of the experiments resulted in transposition of IS 1096; however, better approaches are needed to improve transposition efficiency.

L2 ANSWER 8 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2000:369845 BIOSIS

DN PREV200000369845

TI Identification of an AraC-like molecule in ***Mycobacterium*** marinum linked to virulence in the goldfish model.

AU Pritchett, C. L. (1); Reimschuessel, R.; Kane, A. (1); ***Trucksis,***
*** M.***

CS (1) University of Maryland, Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology,
(2000) Vol. 100, pp. 96. print.

Meeting Info.: 100th General Meeting of the American Society for
Microbiology Los Angeles, California, USA May 21-25, 2000 American Society
for Microbiology
. ISSN: 1060-2011.

DT Conference

LA English

SL English

L2 ANSWER 9 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

DUPLICATE 3

AN 1999:296926 BIOSIS

DN PREV199900296926

TI Superoxide production in phagocytes obtained from ***Mycobacterium***
marinum-stimulated goldfish (Carassius auratus) that were exposed to
copper.

AU Jacobson, Susanne V. (1); ***Trucksis, Michele*** ; Kane, Andrew S.;
Reimschuessel, Renate

CS (1) H. John Heinz III Center for Science, Economics, and the Environment,
1001 Pennsylvania Ave NW, Ste 735 S, Washington, DC, 20004 USA

SO American Journal of Veterinary Research, (June, 1999) Vol. 60, No. 6, pp.
669-675.

ISSN: 0002-9645.

DT Article

LA English

SL English

AB Objective-To investigate the effects of copper exposure and recovery from
copper toxicosis on the nonspecific immune response in
Mycobacterium marinum-inoculated goldfish. Animals-Goldfish
(Carassius auratus) with a mean weight of 33.5 g. Procedure-Superoxide
(O₂-) production was measured in fish 2 to 6 weeks after injection with
phosphate-buffered saline (PBS) solution or M marinum (10² to 10⁷
colony-forming units (CFU)/fish). Then, paired groups of fish were
injected with PBS solution or 10⁴ CFU of M marinum and exposed to copper
(100 mug/L) for 7 days or for 4 days with 3 days of recovery. One paired
group not exposed 14 days later to copper served as control fish.
Phagocyte production of O₂- was measured by use of the nitroblue
tetrazolium reduction assay. Inflammation and bacterial colony counts were
determined by use of routine histologic and microbiologic procedures.
Results-Superoxide production achieved a maximal response 2 to 4 weeks
after M marinum inoculation. Compared with control fish, O₂- production
increased in the groups exposed to copper but then decreased in the
exposed groups that were allowed to recover. Superoxide response and
peritoneal inflammation were greater in M marinum-inoculated groups than
in non-inoculated groups. Conclusions-Copper exposure and inoculation with
M marinum increased O₂- production, whereas recovery after exposure
decreased O₂- production, even in fish that were immunostimulated by M
marinum. Clinical Relevance-When the antimicrobial oxidative response is
suppressed after copper exposure, steps should be taken to avoid imposing
additional stress and minimize the possibility of resurgent or secondary
pathogenic infections.

L2 ANSWER 10 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4

AN 1999:220746 BIOSIS

DN PREV199900220746

TI Pathogenicity of ***Mycobacterium*** fortuitum and
Mycobacterium smegmatis to goldfish, *Carassius auratus*.

AU Talaat, Adel M.; ***Trucksis, Michele*** ; Kane, Andrew S.;
Reimschuessel, Renate (1)

CS (1) Center for Veterinary Medicine, Office of Research, Food and Drug
Administration, 4801 Muirkirk Road, Laurel, MD, 20708 USA

SO Veterinary Microbiology, (April 1, 1999) Vol. 66, No. 2, pp. 151-164.
ISSN: 0378-1135.

DT Article

LA English

SL English

AB Despite the ubiquitous presence of atypical ***mycobacteria*** in the
environment and the potential risk of infection in humans and animals, the
pathogenesis of diseases caused by infection with atypical
mycobacteria has been poorly characterized. In this study,
goldfish, *Carassius auratus* were infected either with the rapidly growing
fish pathogen, ***Mycobacterium*** fortuitum or with another rapidly
growing ***mycobacteria***, ***Mycobacterium*** smegmatis.
Bacterial persistence and pathological host response to
mycobacterial infection in the goldfish are described.
Mycobacteria were recovered from a high percentage of inoculated
fish that developed a characteristic chronic granulomatous response
similar to that associated with natural ***mycobacterial*** infection.
Both *M. fortuitum* and *M. smegmatis* were pathogenic to fish. Fish infected
with *M. smegmatis* ATCC 19420 showed the highest level of giant cell
recruitment compared to fish inoculated with *M. smegmatis* mc2155 and *M.*
fortuitum. Of the three strains of ***mycobacteria*** examined, *M.*
smegmatis ATCC 19420 was the most virulent strain to goldfish followed by
M. fortuitum and *M. smegmatis* mc2155, respectively.

L2 ANSWER 11 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1999:324649 BIOSIS

DN PREV199900324649

TI Use of signature-tagged mutagenesis to identify ***Mycobacterium***
marinum genes required for in vivo survival in the goldfish model of
mycobacterial infection.

AU Talaat, A. (1); Ruley, K. (1); Reimschuessel, R. (1); ***Trucksis, M.***

CS (1) University of Maryland, Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology,
(1999) Vol. 99, pp. 31-32.

Meeting Info.: 99th General Meeting of the American Society for
Microbiology Chicago, Illinois, USA May 30-June 3, 1999 American Society
for Microbiology
ISSN: 1060-2011.

DT Conference

LA English

L2 ANSWER 12 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 5

AN 1998:304726 BIOSIS

DN PREV199800304726

TI Goldfish, *Carassius auratus*, a novel animal model for the study of
Mycobacterium *marinum* pathogenesis.

AU Talaat, Adel M.; Reimschuessel, Renate; Wasserman, Steven S.;
Trucksis, Michele (1)

CS (1) Center Vaccine Development, Div. Geographic Med., Univ. Maryland Sch.

Med., 685 W. Baltimore St., Baltimore, MD 21201 USA
SO Infection and Immunity, (June, 1998) Vol. 66, No. 6, pp. 2938-2942.
ISSN: 0019-9567.

DT Article

LA English

AB We have developed an animal model for studying ***mycobacterial*** pathogenesis using ***Mycobacterium*** marinum and the goldfish, Carassius auratus. Goldfish are injected intraperitoneally with doses between 102 and 109 CFU of M. marinum organisms. Depending on the dose of M. marinum organisms administered, an acute or chronic disease is produced. The acute disease is characterized by systemic ***mycobacterial*** infection, severe peritonitis, tissue necrosis, and a short median survival time. The chronic disease is characterized by granuloma formation in all organs and survival of animals to the end point of the experiment (56 days). Colony counts in organ homogenates showed recovery of ***mycobacteria*** from a high percentage of inoculated animals. We believe this well-characterized animal model will be useful for studying ***mycobacterial*** pathogenesis.

L2 ANSWER 13 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1998:418196 BIOSIS

DN PREV199800418196

TI Optimization of ***Mycobacterium*** marinum transposition.

AU Talaat, A. M.; ***Trucksis, M.***

CS Cent. Vaccine Dev., Univ. Maryland, Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (1998) Vol. 98, pp. 501.

Meeting Info.: 98th General Meeting of the American Society for Microbiology Atlanta, Georgia, USA May 17-21, 1998 American Society for Microbiology

. ISSN: 1060-2011.

DT Conference

LA English

L2 ANSWER 14 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1997:284818 BIOSIS

DN PREV199799584021

TI ***Mycobacterium*** marinum and goldfish, Carassius auratus, A model system for ***mycobacterial*** pathogenesis.

AU Talaat, A.; Deng, Y.; Reimschuessel, R.; ***Trucksis, M.***

CS Univ. Maryland Sch. Med., Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (1997) Vol. 97, No. 0, pp. 562.

Meeting Info.: 97th General Meeting of the American Society for Microbiology Miami Beach, Florida, USA May 4-8, 1997

ISSN: 1060-2011.

DT Conference; Abstract; Conference

LA English

L2 ANSWER 15 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6

AN 1998:78984 BIOSIS

DN PREV199800078984

TI Identification of ***mycobacteria*** infecting fish to the species level using polymerase chain reaction and restriction enzyme analysis.

AU Talaat, Adel M.; Reimschuessel, Renate; ***Trucksis, Michele (1)***

CS (1) Cent. Vaccine Dev., Div. Geographic Med., Univ. Md. Sch. Med., 685 W. Baltimore Street, Baltimore, MD 21201 USA

SO Veterinary Microbiology, (Nov., 1997) Vol. 58, No. 2-4, pp. 229-237.

ISSN: 0378-1135.

DT Article

LA English

AB An assay is described utilizing PCR technology for a rapid diagnostic test to identify fish infection with ***Mycobacterium*** marinum, M. fortuitum and M. chelonae. A 924 bp DNA fragment from a highly conserved area of the ***mycobacterial*** 16S rRNA gene was amplified using ***mycobacteria*** genus-specific primers and digested with restriction enzymes (BamI and ApaI). This examination yielded unique restriction patterns for each ***mycobacterial*** specie enabling identification of ***mycobacteria*** infecting fish to the species level. The protocol can be applied to purified DNA, a simple colony preparation or infected fish tissue. This protocol can be completed in 1-2 days.

L2 ANSWER 16 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1996:259152 BIOSIS

DN PREV199698815281

TI Goldfish, Carassius auratus a fish model for ***mycobacterial*** disease.

AU Talaat, A. (1); Reimschuessel, R.; ***Trucksis, M.***

CS (1) Cent. Vaccine Dev., Univ. Md., Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (1996) Vol. 96, No. 0, pp. 132.

Meeting Info.: 96th General Meeting of the American Society for Microbiology New Orleans, Louisiana, USA May 19-23, 1996
ISSN: 1060-2011.

DT Conference

LA English

L2 ANSWER 17 OF 18 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1995:290086 BIOSIS

DN PREV199598304386

TI The detection of pathogenic fish ***mycobacterium*** using polymerase chain reaction.

AU Talaat, A. (1); Reimschuessel, R.; ***Trucksis, M.***

CS (1) Cent. Vaccine Dev., Univ. Md. Baltimore, Baltimore, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (1995) Vol. 95, No. 0, pp. 132.

Meeting Info.: 95th General Meeting of the American Society for Microbiology Washington, D.C., USA May 21-25, 1995
ISSN: 1060-2011.

DT Conference

LA English

L2 ANSWER 18 OF 18 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 89:288865 SCISEARCH

GA The Genuine Article (R) Number: U8924

TI A 25-YEAR-OLD WOMAN WITH A RIGHT PULMONARY DENSITY 14 MONTHS AFTER A RIGHT UPPER LOBECTOMY FOR AN ATYPICAL CARCINOID-TUMOR - PNEUMONIA AND LYMPHADENITIS DUE TO ***MYCOBACTERIUM*** -AVIUM COMPLEX - ATYPICAL CARCINOID-TUMOR OF BRONCHUS, RESECTE

AU DALY B D T (Reprint); SHEPARD J O; MARK E J; GRILLO H C; POMERANTZ R J; ***TRUCKSIS M***

CS NEW ENGLAND MED CTR, LUNG TUMOR EVALUAT CLIN, BOSTON, MA, 02111 (Reprint); TUFTS UNIV, SCH MED, BOSTON, MA, 02111

CYA USA

SO NEW ENGLAND JOURNAL OF MEDICINE, (1989) Vol. 320, No. 23, pp. 1540-1550.

DT Discussion; Journal

FS LIFE; CLIN

LA ENGLISH

REC Reference Count: 84

=> s tuberculosis and (virulence gene?)

5 FILES SEARCHED...

L3 276 TUBERCULOSIS AND (VIRULENCE GENE?)

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 194 DUP REM L3 (82 DUPLICATES REMOVED)

=> d bib 1-

YOU HAVE REQUESTED DATA FROM 194 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2003:417772 CAPLUS

DN 139:2114

TI ***Virulence*** ***genes*** and proteins from Yersinia pestis,
their use in therapy and screening for antimicrobial drugs

IN Karlyshev, Andrey Vladimirovich; Wren, Brendan William

PA London School of Hygiene and Tropical Medicine, UK

SO PCT Int. Appl., 130 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO	2003044047	A2	20030530	WO	2002-GB5212	20021118
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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT,
TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ,
MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
NE, SN, TD, TG

PRAI GB 2001-27657 A 20011119

L4 ANSWER 2 OF 194 USPATFULL on STN

AN 2003:271146 USPATFULL

TI Minicell-producing parent cells

IN Surber, Mark W., Coronado, CA, UNITED STATES

Sabbadini, Roger A., Lakeside, CA, UNITED STATES

Segall, Anca M., San Diego, CA, UNITED STATES

Berkley, Neil, San Diego, CA, UNITED STATES

PI US 2003190749 A1 20031009

AI US 2002-157215 A1 20020528 (10)

RLI Division of Ser. No. US 2002-154951, filed on 24 May 2002, PENDING

PRAI US 2002-359843P 20020225 (60)

US 2001-293566P 20010524 (60)

DT Utility

FS APPLICATION

LREP KNOBBE MARTENS OLSON & BEAR LLP, 2040 MAIN STREET, FOURTEENTH FLOOR,
IRVINE, CA, 92614

CLMN Number of Claims: 20

ECL Exemplary Claim: 1

DRWN 2 Drawing Page(s)

LN.CNT 18577

L4 ANSWER 3 OF 194 USPATFULL on STN

AN 2003:271080 USPATFULL
TI Minicell-based rational drug design
IN Sabbadini, Roger A., Lakeside, CA, UNITED STATES
Surber, Mark W., Coronado, CA, UNITED STATES
PI US 2003190683 A1 20031009
AI US 2002-157302 A1 20020528 (10)
RLI Division of Ser. No. US 2002-154951, filed on 24 May 2002, PENDING
PRAI US 2002-359843P 20020225 (60)
US 2001-293566P 20010524 (60)
DT Utility
FS APPLICATION
LREP KNOBBE MARTENS OLSON & BEAR LLP, 2040 MAIN STREET, FOURTEENTH FLOOR,
IRVINE, CA, 92614
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 18539

L4 ANSWER 4 OF 194 USPATFULL on STN
AN 2003:270998 USPATFULL
TI Target display on minicells
IN Sabbadini, Roger A., Lakeside, CA, UNITED STATES
Berkley, Neil, San Diego, CA, UNITED STATES
Surber, Mark W., Coronada, CA, UNITED STATES
PI US 2003190601 A1 20031009
AI US 2002-157096 A1 20020528 (10)
RLI Division of Ser. No. US 2002-154951, filed on 24 May 2002, PENDING
PRAI US 2002-359843P 20020225 (60)
US 2001-293566P 20010524 (60)
DT Utility
FS APPLICATION
LREP KNOBBE MARTENS OLSON & BEAR LLP, 2040 MAIN STREET, FOURTEENTH FLOOR,
IRVINE, CA, 92614
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 18581

L4 ANSWER 5 OF 194 USPATFULL on STN
AN 2003:265266 USPATFULL
TI Modified tetracycline repressor protein compositions and methods of use
IN Hillen, Wolfgang, Uttenreuth, GERMANY, FEDERAL REPUBLIC OF
PI US 2003186281 A1 20031002
AI US 2002-326671 A1 20021220 (10)
PRAI US 2001-343278P 20011221 (60)
DT Utility
FS APPLICATION
LREP PENNIE AND EDMONDS, 1155 AVENUE OF THE AMERICAS, NEW YORK, NY, 100362711
CLMN Number of Claims: 35
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 6339

L4 ANSWER 6 OF 194 USPATFULL on STN
AN 2003:265236 USPATFULL
TI Genome sequence tags
IN Dunn, John J., Bellport, NY, UNITED STATES
Van der Lelie, Daniel, Shoreham, NY, UNITED STATES
Krause, Maureen K., Quogue, NY, UNITED STATES
PA Brookhaven Science Associates, LLC, Upton, NY, UNITED STATES, 11973-5000
(U.S. corporation)

PI US 2003186251 A1 20031002
AI US 2002-113916 A1 20020401 (10)
DT Utility
FS APPLICATION
LREP BROOKHAVEN SCIENCE ASSOCIATES/, BROOKHAVEN NATIONAL LABORATORY, BLDG.
475D - P.O. BOX 5000, UPTON, NY, 11973
CLMN Number of Claims: 1
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 919

L4 ANSWER 7 OF 194 USPATFULL on STN
AN 2003:264826 USPATFULL
TI Induction of tumor immunity by variants of folate binding protein
IN Ioannides, Constantin J., Houston, TX, UNITED STATES
Peoples, George E., Fulton, MD, UNITED STATES
PI US 2003185840 A1 20031002
AI US 2002-94097 A1 20020308 (10)
PRAI US 2001-274676P 20010309 (60)
DT Utility
FS APPLICATION
LREP FULBRIGHT & JAWORSKI, LLP, 1301 MCKINNEY; SUITE 5100, HOUSTON, TX,
77010-3095
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 4486

L4 ANSWER 8 OF 194 USPATFULL on STN
AN 2003:257280 USPATFULL
TI Method for identifying helicobacter antigens
IN Meyer, Thomas F, Berlin, GERMANY, FEDERAL REPUBLIC OF
Jungblut, Peter, Berlin, GERMANY, FEDERAL REPUBLIC OF
Baumann, Dirk, Berlin, GERMANY, FEDERAL REPUBLIC OF
Aebischer, Anton, Berlin, GERMANY, FEDERAL REPUBLIC OF
Haas, Gaby, Berlin, GERMANY, FEDERAL REPUBLIC OF
Zimny-Arndt, Ursula, Berlin, GERMANY, FEDERAL REPUBLIC OF
Lamer, Stephanie, Berlin, GERMANY, FEDERAL REPUBLIC OF
Karaali, Galip, Berlin, GERMANY, FEDERAL REPUBLIC OF
Sabarth, Nicolas, Berlin, GERMANY, FEDERAL REPUBLIC OF
Wendland, Meike, Berlin, GERMANY, FEDERAL REPUBLIC OF
PI US 2003180330 A1 20030925
AI US 2003-257976 A1 20030429 (10)
WO 2001-EP4728 20010426
PRAI EP 2000-108968 20000427
EP 2001-101439 20010123
DT Utility
FS APPLICATION
LREP ROTHWELL, FIGG, ERNST & MANBECK, P.C., 1425 K STREET, N.W., SUITE 800,
WASHINGTON, DC, 20005
CLMN Number of Claims: 38
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 3651

L4 ANSWER 9 OF 194 USPATFULL on STN
AN 2003:245149 USPATFULL
TI Regulators of bacterial virulence factor expression
IN McNamara, Peter J., Madison, WI, UNITED STATES
PI US 2003171563 A1 20030911
AI US 2002-145602 A1 20020513 (10)

PRAI US 2001-291917P 20010518 (60)
DT Utility
FS APPLICATION
LREP SENNIGER POWERS LEAVITT AND ROEDEL, ONE METROPOLITAN SQUARE, 16TH FLOOR,
ST LOUIS, MO, 63102
CLMN Number of Claims: 51
ECL Exemplary Claim: 1
DRWN 12 Drawing Page(s)
LN.CNT 4524
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 10 OF 194 USPATFULL on STN
AN 2003:244865 USPATFULL
TI Methods and composition concerning herpesvirus Us3 and BAD-involved
apoptosis
IN Munger, Joshua, Chicago, IL, UNITED STATES
Roizman, Bernard, Chicago, IL, UNITED STATES
PI US 2003171279 A1 20030911
AI US 2002-209967 A1 20020731 (10)
PRAI US 2001-308929P 20010731 (60)
DT Utility
FS APPLICATION
LREP Charles P. Landrum, FULBRIGHT & JAWORSKI L.L.P., SUITE 2400, 600
CONGRESS AVENUE, AUSTIN, TX, 78701-3271
CLMN Number of Claims: 83
ECL Exemplary Claim: 1
DRWN 4 Drawing Page(s)
LN.CNT 6432
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 11 OF 194 USPATFULL on STN
AN 2003:238399 USPATFULL
TI SEMA3B inhibits tumor growth and induces apoptosis in cancer cells
IN Minna, John, Dallas, TX, UNITED STATES
Tomizawa, Yoshio, Takasaki, JAPAN
Sekido, Yoshitaka, Tempaku, JAPAN
Lerman, Michael, Rockville, MD, UNITED STATES
PA Board of Regents, The University of Texas System (non-U.S. corporation)
PI US 2003166557 A1 20030904
AI US 2002-285351 A1 20021031 (10)
PRAI US 2001-335783P 20011031 (60)
DT Utility
FS APPLICATION
LREP Steven L. Highlander, Fulbright & Jaworski L.L.P., Suite 2400, 600
Congress Avenue, Austin, TX, 78701
CLMN Number of Claims: 132
ECL Exemplary Claim: 1
DRWN 15 Drawing Page(s)
LN.CNT 4934
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 12 OF 194 USPATFULL on STN
AN 2003:238122 USPATFULL
TI Minicell-based transfection
IN Sabbadini, Roger A., Lakeside, CA, UNITED STATES
Berkley, Neil, San Diego, CA, UNITED STATES
PI US 2003166279 A1 20030904
AI US 2002-157391 A1 20020528 (10)
RLI Division of Ser. No. US 2002-154951, filed on 24 May 2002, PENDING
PRAI US 2002-359843P 20020225 (60)
US 2001-293566P 20010524 (60)

DT Utility
FS APPLICATION
LREP KNOBBE MARTENS OLSON & BEAR LLP, 2040 MAIN STREET, FOURTEENTH FLOOR,
IRVINE, CA, 92614
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 18548

L4 ANSWER 13 OF 194 USPATFULL on STN
AN 2003:237942 USPATFULL
TI Minicells comprising membrane proteins
IN Sabbadini, Roger A., Lakeside, CA, UNITED STATES
Surber, Mark W., Coronado, CA, UNITED STATES
Berkley, Neil, San Diego, CA, UNITED STATES
Segall, Anca M., San Diego, CA, UNITED STATES
Klepper, Robert, San Diego, CA, UNITED STATES
PI US 2003166099 A1 20030904
AI US 2002-157305 A1 20020528 (10)
PRAI US 2001-295566P 20010605 (60)
US 2002-359843P 20020225 (60)

DT Utility
FS APPLICATION
LREP KNOBBE MARTENS OLSON & BEAR LLP, 2040 MAIN STREET, FOURTEENTH FLOOR,
IRVINE, CA, 92614
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 18580

L4 ANSWER 14 OF 194 USPATFULL on STN
AN 2003:232490 USPATFULL
TI Novel antimicrobial therapies
IN Kornberg, Arthur, Portola Valley, CA, UNITED STATES
PI US 2003162691 A1 20030828
AI US 2003-386246 A1 20030310 (10)
RLI Division of Ser. No. US 2001-896919, filed on 28 Jun 2001, ABANDONED
Continuation-in-part of Ser. No. US 1999-293673, filed on 16 Apr 1999,
ABANDONED
PRAI US 1998-82153P 19980417 (60)

DT Utility
FS APPLICATION
LREP BOZICEVIC, FIELD & FRANCIS LLP, 200 MIDDLEFIELD RD, SUITE 200, MENLO
PARK, CA, 94025
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 10 Drawing Page(s)
LN.CNT 1270
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 15 OF 194 USPATFULL on STN
AN 2003:213265 USPATFULL
TI Method of stimulating and immune response by administration of host
organisms that express intimin alone or as a fusion protein with one of
more other antigens
IN Stewart, C. Neal, JR., Greensboro, NC, UNITED STATES
McKee, Marian L., Great Falls, VA, UNITED STATES
O'Brien, Alison D., Bethesda, MD, UNITED STATES
Wachtel, Marian R., Albany, CA, UNITED STATES
PA Henry M. Jackson Foundation for the Advancement of Military Medicine
(U.S. corporation)

PI US 2003147902 A1 20030807
AI US 2002-150058 A1 20020520 (10)
RLI Division of Ser. No. US 2000-696188, filed on 26 Oct 2000, GRANTED, Pat.
No. US 6406885 Division of Ser. No. US 1997-840466, filed on 18 Apr
1997, GRANTED, Pat. No. US 6261561
PRAI US 1996-15938P 19960422 (60)
US 1996-15657P 19960419 (60)
DT Utility
FS APPLICATION
LREP FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP, 1300 I STREET, NW,
WASHINGTON, DC, 20005
CLMN Number of Claims: 36
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 3124
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 16 OF 194 USPATFULL on STN
AN 2003:207200 USPATFULL
TI Methods for attenuation of virulence in bacteria
IN Mitchell, Wayne, San Francisco, CA, UNITED STATES
Cota, Adam, Berkeley, CA, UNITED STATES
Robert, T. Guy, Oakland, CA, UNITED STATES
PA Tao Biosciences, LLC (U.S. corporation)
PI US 2003143558 A1 20030731
AI US 2002-157736 A1 20020528 (10)
PRAI US 2001-293770P 20010525 (60)
DT Utility
FS APPLICATION
LREP QUINE INTELLECTUAL PROPERTY LAW GROUP, P.C., P O BOX 458, ALAMEDA, CA,
94501
CLMN Number of Claims: 57
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 2794
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 17 OF 194 USPATFULL on STN
AN 2003:200828 USPATFULL
TI Method of diagnosis and disease risk assessment
IN Engstrand, Lars, Uppsala, SWEDEN
Alderborn, Anders, Uppsala, SWEDEN
PI US 2003138813 A1 20030724
AI US 2002-253055 A1 20020924 (10)
PRAI CA 2001-2357572 20010924
US 2001-324681P 20010925 (60)
DT Utility
FS APPLICATION
LREP DORSEY & WHITNEY LLP, INTELLECTUAL PROPERTY DEPARTMENT, 250 PARK AVENUE,
NEW YORK, NY, 10177
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 9 Drawing Page(s)
LN.CNT 1036
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 18 OF 194 USPATFULL on STN
AN 2003:194142 USPATFULL
TI D-alanine racemase mutants of mycobacteria and uses therefore
IN Barletta, Raul G., Lincoln, NE, UNITED STATES
Barletta-Chacon, Ofelia, Lincoln, NE, UNITED STATES

PI US 2003133952 A1 20030717
AI US 2002-323351 A1 20021218 (10)
PRAI US 2001-341485P 20011218 (60)
DT Utility
FS APPLICATION
LREP STINSON MORRISON HECKER LLP, ATTN: PATENT GROUP, 1201 WALNUT STREET,
SUITE 2800, KANSAS CITY, MO, 64106-2150
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1398
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 19 OF 194 USPATFULL on STN
AN 2003:187811 USPATFULL
TI Comparative mycobacterial genomics as a tool for identifying targets for
the diagnosis, prophylaxis or treatment of mycobacterioses
IN Cole, Stewart T., Clamart, FRANCE
PI US 2003129601 A1 20030710
AI US 2002-80170 A1 20020222 (10)
PRAI US 2001-270123P 20010222 (60)
DT Utility
FS APPLICATION
LREP FINNEGAN, HENDERSON, FARABOW, GARRETT &, DUNNER LLP, 1300 I STREET, NW,
WASHINGTON, DC, 20006
CLMN Number of Claims: 74
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 6691
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 20 OF 194 USPATFULL on STN
AN 2003:180679 USPATFULL
TI Method of generating conditionally expressed mutant cells using
expressible antisense sequences
IN Marra, Andrea, Menlo Park, CA, UNITED STATES
Rosenberg, Martin, Royersford, PA, UNITED STATES
Ji, Yinduo, Spring City, PA, UNITED STATES
PA SmithKline Beecham Corporation (U.S. corporation)
PI US 2003124507 A1 20030703
AI US 2002-99198 A1 20020313 (10)
RLI Continuation of Ser. No. US 2000-581479, filed on 25 May 2000, ABANDONED
A 371 of International Ser. No. WO 1998-US25808, filed on 4 Dec 1998,
PENDING
PRAI US 1997-67446P 19971204 (60)
US 1998-82534P 19980420 (60)
US 1998-105161P 19981021 (60)
DT Utility
FS APPLICATION
LREP GLAXOSMITHKLINE, Corporate Intellectual Property - UW2220, P.O. Box
1539, King of Prussia, PA, 19406-0939
CLMN Number of Claims: 16
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 1362
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 21 OF 194 USPATFULL on STN
AN 2003:173169 USPATFULL
TI Identification of essential genes of *Aspergillus fumigatus* and methods
of use

IN Jiang, Bo, Montreal, CANADA
Tishkoff, Daniel, San Diego, CA, UNITED STATES
Zamudio, Carlos, La Jolla, CA, UNITED STATES
Eroshkin, Alexey M., San Diego, CA, UNITED STATES
Hu, Wenqi, Dollard-des-Ormeaux, CANADA
Lemieux, Sebastien, Montreal, CANADA
PI US 2003119013 A1 20030626
AI US 2002-128714 A1 20020423 (10)
PRAI US 2001-316362P 20010831 (60)
US 2001-303899P 20010709 (60)
US 2001-295890P 20010605 (60)
US 2001-287066P 20010427 (60)
US 2001-285697P 20010423 (60)
DT Utility
FS APPLICATION
LREP PENNIE AND EDMONDS, 1155 AVENUE OF THE AMERICAS, NEW YORK, NY, 100362711
CLMN Number of Claims: 43
ECL Exemplary Claim: 1
DRWN 1 Drawing Page(s)
LN.CNT 8519
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 22 OF 194 USPATFULL on STN
AN 2003:173152 USPATFULL
TI Identification of virulence determinants activators in prokaryotic pathogens
IN Murphy, John R., Boston, MA, UNITED STATES
Sun, Li, Old Marston, UNITED KINGDOM
PI US 2003118996 A1 20030626
AI US 2001-971884 A1 20011005 (9)
RLI Division of Ser. No. US 1999-408618, filed on 30 Sep 1999, GRANTED, Pat.
No. US 6309817
PRAI US 1998-102545P 19980930 (60)
DT Utility
FS APPLICATION
LREP LERNER, DAVID, LITTENBERG,, KRUMHOLZ & MENTLIK, 600 SOUTH AVENUE WEST,
WESTFIELD, NJ, 07090
CLMN Number of Claims: 25
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 1386
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 23 OF 194 USPATFULL on STN
AN 2003:166541 USPATFULL
TI Human and mouse choline transporter cDNA
IN Blakely, Randy D., Brentwood, TN, UNITED STATES
Apparsundaram, Subramaniam, Lexington, KY, UNITED STATES
Ferguson, Shawn, Nashville, TN, UNITED STATES
PI US 2003114399 A1 20030619
AI US 2001-911077 A1 20010723 (9)
DT Utility
FS APPLICATION
LREP Priya D. Subramony, FULBRIGHT & JAWORSKI L.L.P., SUITE 2400, 600
CONGRESS AVENUE, AUSTIN, TX, 78701
CLMN Number of Claims: 105
ECL Exemplary Claim: 1
DRWN 17 Drawing Page(s)
LN.CNT 5821
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 24 OF 194 USPATFULL on STN
AN 2003:165439 USPATFULL
TI Compositions and methods for delivery of an agent using attenuated
Salmonella containing phage
IN Bermudes, David G., Wallingford, CT, UNITED STATES
King, Ivan C., North Haven, CT, UNITED STATES
Clairmont, Caroline A., Cheshire, CT, UNITED STATES
PA Vion Pharmaceuticals, Inc. (U.S. corporation)
PI US 2003113293 A1 20030619
AI US 2002-76117 A1 20020213 (10)
RLI Continuation of Ser. No. US 2000-645418, filed on 24 Aug 2000, ABANDONED
PRAI US 1999-150928P 19990826 (60)
DT Utility
FS APPLICATION
LREP PENNIE AND EDMONDS, 1155 AVENUE OF THE AMERICAS, NEW YORK, NY, 100362711
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 7 Drawing Page(s)
LN.CNT 2322
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 25 OF 194 USPATFULL on STN
AN 2003:159307 USPATFULL
TI Tumor suppressor-like proteins that bind IGFBP2
IN Zhang, Wei, Houston, TX, UNITED STATES
Song, Wei Sonya, Houston, TX, UNITED STATES
Fuller, Greg, Houston, TX, UNITED STATES
PI US 2003108920 A1 20030612
AI US 2002-237566 A1 20020909 (10)
PRAI US 2001-318200P 20010907 (60)
DT Utility
FS APPLICATION
LREP Priya D. Subramony, Fulbright & Jaworski L.L.P., Suite 2400, 600
Congress Avenue, Austin, TX, 78701
CLMN Number of Claims: 87
ECL Exemplary Claim: 1
DRWN 4 Drawing Page(s)
LN.CNT 5342
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 26 OF 194 USPATFULL on STN
AN 2003:134810 USPATFULL
TI Polynucleotide functionally coding for the LHP protein from
Mycobacterium ***tuberculosis***, its biologically active derivative
fragments, as well as methods using the same
IN Gicquel, Brigitte, Paris, FRANCE
Berthet, Francois-Xavier, Paris, FRANCE
Anderson, Peter, Bronshoj, DENMARK
Rasmussen, Peter Birk, Bergsgade, DENMARK
PA INSTITUT PASTEUR, Paris Cedex, FRANCE (non-U.S. corporation)
PI US 2003092899 A1 20030515
AI US 2002-140045 A1 20020508 (10)
RLI Division of Ser. No. US 1998-116492, filed on 16 Jul 1998, GRANTED, Pat.
No. US 6436409
PRAI US 1997-52631P 19970716 (60)
DT Utility
FS APPLICATION
LREP OBLON SPIVAK MCCLELLAND MAIER & NEUSTADT PC, FOURTH FLOOR, 1755
JEFFERSON DAVIS HIGHWAY, ARLINGTON, VA, 22202
CLMN Number of Claims: 55
ECL Exemplary Claim: 1

DRWN 14 Drawing Page(s)

LN.CNT 2572

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 27 OF 194 USPATFULL on STN

AN 2003:134564 USPATFULL

TI Method for inhibition of pathogenic microorganisms

IN Kisich, Kevin, Lafayette, CO, UNITED STATES

Diamond, Gill, Short Hills, NJ, UNITED STATES

PA National Jewish Medical & Research Center & University of Medicine &
Dentistry of New Jersey. (U.S. corporation)

PI US 2003092653 A1 20030515

AI US 2002-134039 A1 20020425 (10)

RLI Continuation of Ser. No. US 2000-672723, filed on 28 Sep 2000, ABANDONED

PRAI US 1999-157348P 19990930 (60)

DT Utility

FS APPLICATION

LREP SHERIDAN ROSS PC, 1560 BROADWAY, SUITE 1200, DENVER, CO, 80202

CLMN Number of Claims: 45

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 1810

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 28 OF 194 USPATFULL on STN

AN 2003:134562 USPATFULL

TI Tissue-specific and target RNA-specific ribozymes

IN Norris, James S., Mt. Pleasant, SC, UNITED STATES

Clawson, Gary A., Bethesda, MD, UNITED STATES

Schmidt, Michael G., Mt. Pleasant, SC, UNITED STATES

Hoel, Brian, Charleston, SC, UNITED STATES

Pan, Wei-Hua, Hummelstown, PA, UNITED STATES

Dolan, Joseph W., Mt. Pleasant, SC, UNITED STATES

Schofield, David, Mt. Pleasant, SC, UNITED STATES

Westwater, Caroline, Charleston, SC, UNITED STATES

Huang, Cancan, Charleston, SC, UNITED STATES

PA Medical University of South Carolina, an agency of the State of South
Carolina (U.S. corporation)

PI US 2003092651 A1 20030515

AI US 2002-82973 A1 20020226 (10)

RLI Continuation of Ser. No. US 1999-338942, filed on 24 Jun 1999, ABANDONED

PRAI US 1998-90560P 19980624 (60)

US 1998-96502P 19980814 (60)

DT Utility

FS APPLICATION

LREP JANIS K. FRASER, PH.D., J.D., Fish & Richardson P.C., 225 Franklin
Street, Boston, MA, 02100-2804

CLMN Number of Claims: 38

ECL Exemplary Claim: 1

DRWN 12 Drawing Page(s)

LN.CNT 2698

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 29 OF 194 USPATFULL on STN

AN 2003:120803 USPATFULL

TI ginS

IN Burgess, Nicola A., Lichfield, UNITED KINGDOM

Garcia, Miguel M. Camara, Chesterfield, UNITED KINGDOM

Kirke, David F., Kimberley, UNITED KINGDOM

Meyers, Nicholas L., Huntingdon, UNITED KINGDOM

Williams, Paul, Kimberley, UNITED KINGDOM

PI US 2003083287 A1 20030501
AI US 2001-998279 A1 20011130 (9)
PRAI US 2000-250288P 20001130 (60)
DT Utility
FS APPLICATION
LREP Edward R. Gimmi, SmithKline Beecham Corporation, Corporate Intellectual
Property -U.S., UW2220, P.O. Box 1539, King of Prussia, PA, 19406-0939
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 19 Drawing Page(s)
LN.CNT 2634
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 30 OF 194 USPATFULL on STN

AN 2003:120785 USPATFULL

TI Nad synthetase inhibitors and uses thereof

IN Brouillette, Wayne J., Pelham, AL, UNITED STATES

DeLucas, Lawrence, Birmingham, AL, UNITED STATES

Brouillette, Christie, Pelham, AL, UNITED STATES

Velu, Sadanandan E., Birmingham, AL, UNITED STATES

Kim, Yong-Chul, Gwangsan-gu, KOREA, REPUBLIC OF

Mou, Liyuan, Birmingham, AL, UNITED STATES

Porter, R. Stephen, Brentwood, TN, UNITED STATES

PA Virtual Drug Development, Inc., Brentwood, TN (U.S. corporation)

PI US 2003083269 A1 20030501

AI US 2002-80279 A1 20020222 (10)

RLI Continuation-in-part of Ser. No. US 2000-617258, filed on 14 Jul 2000,
PENDING Continuation of Ser. No. WO 1999-US14839, filed on 30 Jun 1999,
PENDING Continuation of Ser. No. WO 1999-US810, filed on 14 Jan 1999,
PENDING Continuation-in-part of Ser. No. US 2000-606256, filed on 29 Jun
2000, PENDING Continuation-in-part of Ser. No. WO 2000-US18029, filed on
29 Jun 2000, PENDING Continuation-in-part of Ser. No. WO 2001-US22203,
filed on 13 Jul 2001, PENDING

PRAI US 1998-97880P 19980825 (60)

US 1998-71399P 19980114 (60)

US 1999-141436P 19990629 (60)

US 2000-218405P 20000714 (60)

DT Utility

FS APPLICATION

LREP Jack B. Hicks, Esq., Womble Carlyle Sandbridge & Rice, PLLC, 300 North
Greene Street, Suite 1900, Greensboro, NC, 27402

CLMN Number of Claims: 85

ECL Exemplary Claim: 1

DRWN 3 Drawing Page(s)

LN.CNT 2707

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 31 OF 194 USPATFULL on STN

AN 2003:120052 USPATFULL

TI Method, compositions and kit for detection of microorganisms and
bi-directional sequencing of nucleic acid polymers

IN Leushner, James, North York, CANADA

Hui, May, Toronto, CANADA

Dunn, James M., Scarborough, CANADA

Lacroix, Jean-Michel, Etobicoke, CANADA

PI US 2003082535 A1 20030501

AI US 2001-802110 A1 20010307 (9)

RLI Continuation of Ser. No. US 1999-311260, filed on 13 May 1999, GRANTED,
Pat. No. US 6214555 Continuation-in-part of Ser. No. US 1998-9483, filed
on 20 Jan 1998, GRANTED, Pat. No. US 6083699 Continuation-in-part of
Ser. No. US 1996-640672, filed on 1 May 1996, GRANTED, Pat. No. US

5789168 Continuation-in-part of Ser. No. US 1996-684498, filed on 19 Jul 1996, GRANTED, Pat. No. US 5830657 Continuation-in-part of Ser. No. US 1997-807138, filed on 27 Feb 1997, GRANTED, Pat. No. US 5888736 Continuation-in-part of Ser. No. WO 1997-US7134, filed on 29 Apr 1997, UNKNOWN

DT Utility
FS APPLICATION
LREP OPPEDAHLL AND LARSON LLP, P O BOX 5068, DILLON, CO, 80435-5068
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1812
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 32 OF 194 USPATFULL on STN

AN 2003:64683 USPATFULL

TI Abundant, well distributed and hyperpolymorphic simple sequence repeats in prokaryote genomes and use of same for prokaryote classification and typing

IN Kashi, Yechezkel, Haifa, ISRAEL
Gur-Arie, Riva, Binyamina, ISRAEL
Cohen, Cyril, Nesher, ISRAEL
Eitan, Yuval, Jerusalem, ISRAEL
Shelef, Leora, Bloommfield Village, MI, UNITED STATES
Hallerman, Eric, Blacksburg, VA, UNITED STATES

PI US 2003044804 A1 20030306

AI US 2001-971894 A1 20011009 (9)

RLI Division of Ser. No. US 1999-472035, filed on 27 Dec 1999, PATENTED

DT Utility

FS APPLICATION

LREP SOL SHEINBEIN, c/o ANTHONY CASTORINA, SUITE 207, 2001 JEFFERSON DAVIS HIGHWAY, ARLINGTON, VA, 22202

CLMN Number of Claims: 51

ECL Exemplary Claim: 1

DRWN 8 Drawing Page(s)

LN.CNT 1851

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 33 OF 194 USPATFULL on STN

AN 2003:44768 USPATFULL

TI Methods and compositions for the treatment of macular and retinal degenerations

IN Travis, Gabriel H., Los Angeles, CA, UNITED STATES
PA Board of Regents, The University of Texas System (U.S. corporation)

PI US 2003032078 A1 20030213

AI US 2001-885303 A1 20010619 (9)

PRAI US 2001-263837P 20010123 (60)

DT Utility

FS APPLICATION

LREP Gina N. Shishima, Fulbright & Jaworski L.L.P., Suite 2400, 600 Congress Avenue, Austin, TX, 78701

CLMN Number of Claims: 53

ECL Exemplary Claim: 1

DRWN 7 Drawing Page(s)

LN.CNT 7372

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 34 OF 194 USPATFULL on STN

AN 2003:44373 USPATFULL

TI Recombinant vaccines comprising immunogenic attenuated bacteria having RpoS positive phenotype

IN Curtiss, Roy, III, St. Louis, MO, UNITED STATES
Nickerson, Cheryl A., River Ridge, LA, UNITED STATES
PI US 2003031683 A1 20030213
AI US 2002-138239 A1 20020503 (10)
RLI Continuation of Ser. No. US 1999-314062, filed on 18 May 1999, GRANTED,
Pat. No. US 6383496 Continuation-in-part of Ser. No. US 1997-970789,
filed on 14 Nov 1997, GRANTED, Pat. No. US 6024961
DT Utility
FS APPLICATION
LREP THOMPSON COBURN, LLP, ONE FIRSTAR PLAZA, SUITE 3500, ST LOUIS, MO, 63101
CLMN Number of Claims: 86
ECL Exemplary Claim: 1
DRWN 16 Drawing Page(s)
LN.CNT 3787
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 35 OF 194 USPATFULL on STN
AN 2003:29854 USPATFULL
TI Method of enhancing T cell immunity by selection of antigen specific T
cells
IN Ignatowicz, Leszek, Evans, GA, UNITED STATES
Kraj, Piotr, Augusta, GA, UNITED STATES
PI US 2003021796 A1 20030130
AI US 2002-137745 A1 20020502 (10)
PRAI US 2001-288867P 20010504 (60)
DT Utility
FS APPLICATION
LREP Charles P. Landrum, FULBRIGHT & JAWORSKI L.L.P., SUITE 2400, 600
CONGRESS AVENUE, AUSTIN, TX, 78701-3271
CLMN Number of Claims: 38
ECL Exemplary Claim: 1
DRWN 17 Drawing Page(s)
LN.CNT 3185
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 36 OF 194 USPATFULL on STN
AN 2003:196946 USPATFULL
TI Immunodeficiency recombinant poxvirus
IN Paoletti, Enzo, Delmar, NY, United States
Tartaglia, James, Schenectady, NY, United States
Cox, William I., East Greenbush, NY, United States
Gallo, Robert, Baltimore, MD, United States
Franchini, Genoveffa, Washington, DC, United States
PA Virogenetics Corporation, Troy, NY, United States (U.S. corporation)
PI US 6596279 B1 20030722
AI US 1998-136159 19980814 (9)
RLI Division of Ser. No. US 1995-417210, filed on 5 Apr 1995, now patented,
Pat. No. US 5863542 Continuation-in-part of Ser. No. US 1994-223842,
filed on 6 Apr 1994, now abandoned Continuation-in-part of Ser. No. US
1992-897382, filed on 11 Jun 1992, now abandoned Continuation-in-part of
Ser. No. US 1991-715921, filed on 14 Jun 1991, now abandoned
Continuation-in-part of Ser. No. US 136159 Continuation-in-part of Ser.
No. US 1993-105483, filed on 12 Aug 1993, now patented, Pat. No. US
5494807 Continuation of Ser. No. US 1992-847951, filed on 6 Mar 1992,
now abandoned Continuation-in-part of Ser. No. US 1991-713967, filed on
11 Jun 1991, now abandoned Continuation-in-part of Ser. No. US
1991-666056, filed on 7 Mar 1991, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: Scheiner, Laurie; Assistant Examiner: Parkin, Jeffrey
S.

LREP Halloran, Patrick J.
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 175 Drawing Figure(s); 128 Drawing Page(s)
LN.CNT 6880
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 37 OF 194 USPATFULL on STN
AN 2003:20108 USPATFULL
TI DNA molecule encoding for cellular uptake of Mycobacterium
tuberculosis and uses thereof
IN Riley, Lee W., New York, NY, United States
PA Cornell Research Foundation, Inc., Ithaca, NY, United States (U.S.
corporation)
PI US 6509151 B1 20030121
AI US 1995-392210 19950222 (8)
RLI Continuation-in-part of Ser. No. US 1993-118442, filed on 2 Sep 1993,
now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Tung, Joyce
LREP Nixon, Hargrave, Devans & Doyle LLP
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 9 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 1525
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 38 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2003:374855 SCISEARCH
GA The Genuine Article (R) Number: 672BT
TI Characterization of the role of the divalent metal ion-dependent
transcriptional repressor MntR in the virulence of Staphylococcus aureus
AU Ando M; Manabe Y C; Converse P J; Miyazaki E; Harrison R; Murphy J R;
Bishai W R (Reprint)
CS Johns Hopkins Univ, Sch Med, Ctr Tuberculosis Res, Dept Med, Div Infect
Dis, 424 N Bond St, Rm 112, Baltimore, MD 21205 USA (Reprint); Johns
Hopkins Univ, Sch Med, Ctr Tuberculosis Res, Dept Med, Div Infect Dis,
Baltimore, MD 21205 USA; Johns Hopkins Univ, Bloomberg Sch Publ Hlth, Dept
Int Hlth, Div Dis Control, Baltimore, MD 21205 USA; Boston Univ, Sch Med,
Dept Med, Sect Mol Med, Boston, MA 02118 USA; Adv Microbial Solut,
Milford, MA USA
CYA USA
SO INFECTION AND IMMUNITY, (MAY 2003) Vol. 71, No. 5, pp. 2584-2590.
Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904
USA.
ISSN: 0019-9567.
DT Article; Journal
LA English
REC Reference Count: 40
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 39 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE I
AN 2003:442379 CAPLUS
TI Trace metals and their relation to bacterial infections studied by X-ray
microscopy
AU Maser, J.; Wagner, D.; Lai, B.; Cai, Z.; Legnini, D.; Moric, I.; Bermudez,
L.
CS Experimental Facilities Division, Argonne National Laboratory, Argonne,
IL, 60439, USA
SO Journal de Physique IV: Proceedings (2003), 104(X-Ray Microscopy), 283-288

CODEN: JPICEI; ISSN: 1155-4339
PB EDP Sciences
DT Journal
LA English
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 40 OF 194 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS
RESERVED. on STN DUPLICATE 2
AN 2003347377 EMBASE
TI Strategies for mycobacterial genetics.
AU Morszeck C.
CS C. Morszeck, Stiftung Caesar, Ludwig-Erhard Allee 2, D-53175 Bonn,
Germany. Morszeck@caesar.de
SO International Journal of Medical Microbiology, (2003) 293/4 (251-259).
Refs: 53
ISSN: 1438-4221 CODEN: IMEMFV
CY Germany
DT Journal; (Short Survey)
FS 004 Microbiology
LA English
SL English

L4 ANSWER 41 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2003:415420 CAPLUS
DN 139:241038
TI Partial genome sequencing of Rhodococcus equi ATCC 33701
AU Rahman, M. T.; Herron, L. L.; Kapur, V.; Meijer, W. G.; Byrne, B. A.; Ren,
J.; Nicholson, V. M.; Prescott, J. F.
CS Department of Pathobiology, University of Guelph, Guelph, N1G 2W1, Can.
SO Veterinary Microbiology (2003), 94(2), 143-158
CODEN: VMICDQ; ISSN: 0378-1135
PB Elsevier Science B.V.
DT Journal
LA English
RE.CNT 68 THERE ARE 68 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 42 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2003:362504 CAPLUS
DN 139:47630
TI Molecular genetics of Mycobacterium ***tuberculosis***
AU Tungusova, O. S.; Mar'yandyshev, A. O.
CS Arkhangel. Gos. Med. Akad., Russia
SO Problemy Tuberkuleza (2003), (2), 43-45
CODEN: PRTUAX; ISSN: 0032-9533
PB Izdatel'stvo Meditsina
DT Journal; General Review
LA Russian

L4 ANSWER 43 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2003:709666 SCISEARCH
GA The Genuine Article (R) Number: 711UP
TI I-TRAP: A method to identify transcriptional regulator activated promoters
AU McLendon M M; Shinnick T M (Reprint)
CS Ctr Dis Control & Prevent, Div AIDS STD & TB Lab Res, Natl Ctr Infect Dis,
Atlanta, GA 30333 USA (Reprint); Emory Univ, Dept Microbiol & Immunol,
Atlanta, GA 30322 USA
CYA USA
SO BMC INFECTIOUS DISEASES, (11 JUL 2003) Vol. 3, am. 15.
Publisher: BIOMED CENTRAL LTD, MIDDLESEX HOUSE, 34-42 CLEVELAND ST, LONDON

WIT 4LB, ENGLAND.

ISSN: 1471-2334.

DT Article; Journal

LA English

REC Reference Count: 23

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 44 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2003:709664 SCISEARCH

GA The Genuine Article (R) Number: 711UJ

TI Lateral Gene Transfer (LGT) between Archaea and Escherichia coli is a contributor to the emergence of novel infectious disease

AU Faguy D M (Reprint)

CS Univ New Mexico, Dept Biol, Albuquerque, NM 87131 USA (Reprint)

CYA USA

SO BMC INFECTIOUS DISEASES, (19 JUN 2003) Vol. 3, am. 13.

Publisher: BIOMED CENTRAL LTD, MIDDLESEX HOUSE, 34-42 CLEVELAND ST, LONDON WIT 4LB, ENGLAND.

ISSN: 1471-2334.

DT Article; Journal

LA English

REC Reference Count: 43

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 45 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2003:629118 CAPLUS

TI I-TRAP: a method to identify transcriptional regulator activated promoters

AU McLendon, Molly M.; Shinnick, Thomas M.

CS Department of Microbiology and Immunology, Emory University, Atlanta, GA, 30322, USA

SO BMC Infectious Diseases (2003), 3, No pp. given

CODEN: BIDMBJ; ISSN: 1471-2334

URL: <http://www.biomedcentral.com/content/pdf/1471-2334-3-15.pdf>

PB BioMed Central Ltd.

DT Journal; (online computer file)

LA English

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 46 OF 194 USPATFULL on STN

AN 2002:336870 USPATFULL

TI Methods of identifying bacterial genes that are incompatible with bacterial pathogenicity, and the use of such genes, such as cadA, to reduce pathogenicity in a bacteria or to combat pathogenic bacterial infections

IN Maurelli, Anthony T., Silver Spring, MD, UNITED STATES

Fernandez, Reinaldo E., Silver Spring, MD, UNITED STATES

Bloch, Craig A., Ann Arbor, MI, UNITED STATES

Fasano, Alessio, West Friendship, MD, UNITED STATES

PI US 2002192225 A1 20021219

AI US 2002-34213 A1 20020103 (10)

RLI Division of Ser. No. US 1999-281274, filed on 30 Mar 1999, GRANTED, Pat.

No. US 6344201

PRAI US 1998-80202P 19980331 (60)

DT Utility

FS APPLICATION

LREP FINNEGAN, HENDERSON, FARABOW, GARRETT &, DUNNER LLP, 1300 I STREET, NW, WASHINGTON, DC, 20005

CLMN Number of Claims: 41

ECL Exemplary Claim: 1

DRWN 5 Drawing Page(s)

LN.CNT 1729

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 47 OF 194 USPATFULL on STN

AN 2002:307566 USPATFULL

TI Methods and compositions for therapeutic intervention in infectious disease

IN Stewart, Graham, Walton-on-Thames, UNITED KINGDOM

O'Gaora, Peadar, London, UNITED KINGDOM

Young, Douglas, Ruislip, UNITED KINGDOM

PI US 2002172685 A1 20021121

AI US 2002-79136 A1 20020220 (10)

PRAI US 2001-269801P 20010220 (60)

US 2001-294170P 20010529 (60)

DT Utility

FS APPLICATION

LREP JOHN S. PRATT, ESQ, KILPATRICK STOCKTON, LLP, 1100 PEACHTREE STREET,
SUITE 2800, ATLANTA, GA, 30309

CLMN Number of Claims: 20

ECL Exemplary Claim: 1

DRWN 15 Drawing Page(s)

LN.CNT 1922

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 48 OF 194 USPATFULL on STN

AN 2002:272939 USPATFULL

TI PEI: DNA vector formulations for in vitro and in vivo gene delivery

IN Cristiano, Richard J., Pearland, TX, UNITED STATES

Yamashita, Motoyuki, Kochi City, JAPAN

PA Board of Regents, The University of Texas System (U.S. corporation)

PI US 2002151060 A1 20021017

AI US 2001-962922 A1 20010925 (9)

PRAI US 2000-235237P 20000925 (60)

US 2000-235635P 20000926 (60)

DT Utility

FS APPLICATION

LREP FULBRIGHT & JAWORSKI L.L.P., A REGISTERED LIMITED LIABILITY PARTNERSHIP,
SUITE 2400, 600 CONGRESS AVENUE, AUSTIN, TX, 78701

CLMN Number of Claims: 141

ECL Exemplary Claim: 1

DRWN 31 Drawing Page(s)

LN.CNT 7002

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 49 OF 194 USPATFULL on STN

AN 2002:221400 USPATFULL

TI Tumor suppressor CAR-1

IN Killary, Ann, West University Place, TX, UNITED STATES

Lott, Steve, Palo Alto, CA, UNITED STATES

Chandler, Dawn, Houston, TX, UNITED STATES

PI US 2002119541 A1 20020829

AI US 2001-927091 A1 20010809 (9)

PRAI US 2000-227560P 20000823 (60)

US 2000-225033P 20000810 (60)

DT Utility

FS APPLICATION

LREP Thomas M. Boyce, FULBRIGHT & JAWORSKI L.L.P., A REGISTERED LIMITED
LIABILITY PARTNERSHIP, 600 CONGRESS AVENUE, SUITE 2400, AUSTIN, TX,
78701

CLMN Number of Claims: 100

ECL Exemplary Claim: 1

DRWN 6 Drawing Page(s)
LN.CNT 8876
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 50 OF 194 USPATFULL on STN
AN 2002:164714 USPATFULL
TI Method of reducing bacterial proliferation
IN Mahan, Michael J., Santa Barbara, CA, UNITED STATES
Heithoff, Douglas M., Goleta, CA, UNITED STATES
Low, David A., Goleta, CA, UNITED STATES
Sinsheimer, Robert L., Santa Barbara, CA, UNITED STATES
PI US 2002086332 A1 20020704
AI US 2001-928227 A1 20010809 (9)
RLI Continuation-in-part of Ser. No. US 2000-612116, filed on 7 Jul 2000,
PENDING Continuation-in-part of Ser. No. US 2000-495614, filed on 1 Feb
2000, PENDING
PRAI US 1999-183043P 19990202 (60)
US 1999-198250P 19990505 (60)
DT Utility
FS APPLICATION
LREP Catherine M. Polizzi, Morrison & Foerster LLP, 755 Page Mill Road, Palo
Alto, CA, 94304-1018
CLMN Number of Claims: 46
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 3811
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 51 OF 194 USPATFULL on STN
AN 2002:164671 USPATFULL
TI GENOMIC PROFILING: A RAPID METHOD FOR TESTING A COMPLEX BIOLOGICAL
SAMPLE FOR THE PRESENCE OF MANY TYPES OF ORGANISMS
IN STRAUS, DON, CAMBRIDGE, MA, UNITED STATES
PI US 2002086289 A1 20020704
AI US 1999-333110 A1 19990615 (9)
DT Utility
FS APPLICATION
LREP PAUL T CLARK, CLARK & ELBING LLP, 176 FEDERAL STREET, BOSTON, MA, 02110
CLMN Number of Claims: 57
ECL Exemplary Claim: 1
DRWN 11 Drawing Page(s)
LN.CNT 3737
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 52 OF 194 USPATFULL on STN
AN 2002:164418 USPATFULL
TI Producing antibodies with attenuated bacteria with altered DNA adenine
methylase activity
IN Mahan, Michael J., Santa Barbara, CA, UNITED STATES
Heithoff, Douglas M., Goleta, CA, UNITED STATES
Low, David A., Goleta, CA, UNITED STATES
Sinsheimer, Robert L., Santa Barbara, CA, UNITED STATES
PI US 2002086032 A1 20020704
AI US 2001-927896 A1 20010809 (9)
RLI Continuation-in-part of Ser. No. US 2000-612116, filed on 7 Jul 2000,
PENDING Continuation-in-part of Ser. No. US 2000-495614, filed on 1 Feb
2000, PENDING
PRAI US 1999-183043P 19990202 (60)
US 1999-198250P 19990505 (60)
DT Utility
FS APPLICATION

LREP Catherine M. Polizzi, Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA, 94304-1018
CLMN Number of Claims: 42
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 3833
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 53 OF 194 USPATFULL on STN
AN 2002:157087 USPATFULL
TI Novel antimicrobial therapies
IN Kornberg, Arthur, Portola Valley, CA, UNITED STATES
PI US 2002081686 A1 20020627
AI US 2001-896919 A1 20010628 (9)
RLI Continuation-in-part of Ser. No. US 1999-293673, filed on 16 Apr 1999, UNKNOWN
DT Utility
FS APPLICATION
LREP Bret E. Field, Bozicevic, Field and Francis LLP, Suite 200, 200 Middlefield Road, Menlo Park, CA, 94025
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 10 Drawing Page(s)
LN.CNT 1266
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 54 OF 194 USPATFULL on STN
AN 2002:156721 USPATFULL
TI Bacteria with altered DNA adenine methylase (DAM) activity and heterologous epitope
IN Mahan, Michael J., Santa Barbara, CA, UNITED STATES
Heithoff, Douglas M., Goleta, CA, UNITED STATES
Low, David A., Goleta, CA, UNITED STATES
Sinsheimer, Robert L., Santa Barbara, CA, UNITED STATES
PI US 2002081317 A1 20020627
AI US 2001-927788 A1 20010809 (9)
RLI Continuation-in-part of Ser. No. US 2000-612116, filed on 7 Jul 2000, PENDING
Continuation-in-part of Ser. No. US 2000-495614, filed on 1 Feb 2000, PENDING
PRAI US 1999-183043P 19990202 (60)
US 1999-198250P 19990505 (60)
DT Utility
FS APPLICATION
LREP Catherine M. Polizzi, Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA, 94304-1018
CLMN Number of Claims: 29
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 3781
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 55 OF 194 USPATFULL on STN
AN 2002:149116 USPATFULL
TI Reducing bacterial virulence
IN Mahan, Michael J., Santa Barbara, CA, UNITED STATES
Heithoff, Douglas M., Goleta, CA, UNITED STATES
Low, David A., Goleta, CA, UNITED STATES
Sinsheimer, Robert L., Santa Barbara, CA, UNITED STATES
PI US 2002077272 A1 20020620
AI US 2001-927885 A1 20010809 (9)
RLI Continuation-in-part of Ser. No. US 2000-612116, filed on 7 Jul 2000,

PENDING Continuation-in-part of Ser. No. US 2000-495614, filed on 1 Feb 2000, PENDING

PRAI US 1999-183043P 19990202 (60)

US 1999-198250P 19990505 (60)

DT Utility

FS APPLICATION

LREP Catherine M. Polizzi, Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA, 94304-1018

CLMN Number of Claims: 44

ECL Exemplary Claim: 1

DRWN 8 Drawing Page(s)

LN.CNT 3809

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 56 OF 194 USPATFULL on STN

AN 2002:148280 USPATFULL

TI Attenuated bacteria with altered DNA adenine methylase activity

IN Mahan, Michael J., Santa Barbara, CA, UNITED STATES

Heithoff, Douglas M., Goleta, CA, UNITED STATES

Low, David A., Goleta, CA, UNITED STATES

Sinsheimer, Robert L., Santa Barbara, CA, UNITED STATES

PI US 2002076417 A1 20020620

AI US 2001-927767 A1 20010809 (9)

RLI Continuation-in-part of Ser. No. US 2000-612116, filed on 7 Jul 2000,
PENDING Continuation-in-part of Ser. No. US 2000-495614, filed on 1 Feb 2000, PENDING

PRAI US 1999-183043P 19990202 (60)

US 1999-198250P 19990505 (60)

DT Utility

FS APPLICATION

LREP Catherine M. Polizzi, Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA, 94304-1018

CLMN Number of Claims: 34

ECL Exemplary Claim: 1

DRWN 8 Drawing Page(s)

LN.CNT 3803

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 57 OF 194 USPATFULL on STN

AN 2002:133219 USPATFULL

TI Method of creating antibodies and compositions used for same

IN Mahan, Michael J., Santa Barbara, CA, UNITED STATES

Heithoff, Douglas M., Goleta, CA, UNITED STATES

Low, David A., Goleta, CA, UNITED STATES

Sinsheimer, Robert L., Santa Barbara, CA, UNITED STATES

PI US 2002068068 A1 20020606

AI US 2001-927765 A1 20010809 (9)

RLI Continuation-in-part of Ser. No. US 2000-612116, filed on 7 Jul 2000,
PENDING Continuation-in-part of Ser. No. US 2000-495614, filed on 1 Feb 2000, PENDING

PRAI US 1999-183043P 19990202 (60)

US 1999-198250P 19990505 (60)

DT Utility

FS APPLICATION

LREP Catherine M. Polizzi, Morrison & Foerster LLP, 755 Page Mill Road, Palo Alto, CA, 94304-1018

CLMN Number of Claims: 34

ECL Exemplary Claim: 1

DRWN 8 Drawing Page(s)

LN.CNT 3795

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 58 OF 194 USPATFULL on STN
AN 2002:126346 USPATFULL
TI COMPOSITIONS INCLUDING GLYCOSAMINOGLYCANS DEGRADING ENZYMES AND USE OF
SAME AGAINST SURFACE PROTECTED BACTERIA
IN YACOBY-ZEEVI, ORON, MEITAR, ISRAEL
PI US 2002064858 A1 20020530
US 6423312 B2 20020723
AI US 1998-140888 A1 19980827 (9)
RLI Continuation of Ser. No. US 1998-46475, filed on 25 Mar 1998, PATENTED
Continuation-in-part of Ser. No. US 1997-922170, filed on 2 Sep 1997,
PATENTED
DT Utility
FS APPLICATION
LREP Sol Steinbein, G. E. Ehrlich Ltd, c/o Anthony Castorina, 2001 Jefferson
Davis Highway Ste. 207, Arlington, VA, 22202
CLMN Number of Claims: 41
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 1131
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 59 OF 194 USPATFULL on STN
AN 2002:209121 USPATFULL
TI Polynucleotide functionally coding for the LHP protein from
Mycobacterium ***tuberculosis***, its biologically active derivative
fragments, as well as methods using the same
IN Gicquel, Brigitte, Paris, FRANCE
Berthet, Francois-Xavier, Paris, FRANCE
Andersen, Peter, Bronshoj, DENMARK
Rasmussen, Peter Birk, Kobehavn, DENMARK
PA Institut Pasteur, Paris, FRANCE (non-U.S. corporation)
PI US 6436409 B1 20020820
AI US 1998-116492 19980716 (9)
PRAI US 1997-52631P 19970716 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Swartz, Rodney P
LREP Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 21 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 2304
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 60 OF 194 USPATFULL on STN
AN 2002:144099 USPATFULL
TI Plants and plant cells expressing histidine tagged intimin
IN Stewart, Jr., C. Neal, Greensboro, NC, United States
McKee, Marian L., Great Falls, VA, United States
O'Brien, Alison D., Bethesda, MD, United States
Wachtel, Marian R., Gaithersburg, MD, United States
PA Henry M. Jackson Foundation for the Advancement of Military Medicine,
Rockville, MD, United States (U.S. corporation)
PI US 6406885 B1 20020618
AI US 2000-696188 20001026 (9)
RLI Division of Ser. No. US 1997-840466, filed on 18 Apr 1997, now patented,
Pat. No. US 6261561
PRAI US 1996-15938P 19960422 (60)
US 1996-15657P 19960419 (60)
DT Utility

FS GRANTED

EXNAM Primary Examiner: Navarro, Mark; Assistant Examiner: Portner, Ginny Allen

LREP Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.

CLMN Number of Claims: 13

ECL Exemplary Claim: 1

DRWN 23 Drawing Figure(s); 23 Drawing Page(s)

LN.CNT 2819

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 61 OF 194 USPATFULL on STN

AN 2002:130091 USPATFULL

TI DNA molecule encoding for cellular uptake of mycobacterium
tuberculosis and uses thereof

IN Riley, Lee W., Berkeley, CA, United States

PA Cornell Research Foundation, Inc, Ithaca, NY, United States (U.S.
corporation)

PI US 6399764 B1 20020604

AI US 2000-574462 20000518 (9)

RLI Division of Ser. No. US 1997-907229, filed on 6 Aug 1997, now patented,
Pat. No. US 6072048

PRAI US 1997-40097P 19970310 (60)

DT Utility

FS GRANTED

EXNAM Primary Examiner: Swartz, Rodney P

LREP Nixon Peabody LLP

CLMN Number of Claims: 9

ECL Exemplary Claim: 1

DRWN 17 Drawing Figure(s); 6 Drawing Page(s)

LN.CNT 1209

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 62 OF 194 USPATFULL on STN

AN 2002:102056 USPATFULL

TI Recombinant vaccines comprising immunogenic attenuated bacteria having
RPOS positive phenotype

IN Curtiss, III, Roy, St. Louis, MO, United States

Nickerson, Cheryl A., River Ridge, LA, United States

PA Washington University, St. Louis, MO, United States (U.S. corporation)

PI US 6383496 B1 20020507

AI US 1999-314062 19990518 (9)

RLI Continuation-in-part of Ser. No. US 1997-970789, filed on 14 Nov 1997,
now patented, Pat. No. US 6024961

DT Utility

FS GRANTED

EXNAM Primary Examiner: Mosher, Mary E.

LREP Thompson Coburn LLP

CLMN Number of Claims: 31

ECL Exemplary Claim: 1,23

DRWN 16 Drawing Figure(s); 16 Drawing Page(s)

LN.CNT 3579

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 63 OF 194 USPATFULL on STN

AN 2002:81259 USPATFULL

TI Recombinant mycobacteria

IN Bloom, Barry R., Hastings on Hudson, NY, United States

Davis, Ronald W., Palo Alto, CA, United States

Jacobs, Jr., William R., Bronx, NY, United States

Young, Richard A., Winchester, MA, United States

Husson, Robert N., Takoma Park, MD, United States

PA Albert Einstein College of Medicine of Yeshiva University, Bronx, NY,
United States (U.S. corporation)

PI US 6372478 B1 20020416

AI US 1999-314207 19990519 (9)

RLI Continuation of Ser. No. US 1998-14560, filed on 28 Jan 1998, now
patented, Pat. No. US 5968733 Continuation of Ser. No. US 1995-463942,
filed on 5 Jun 1995, now patented, Pat. No. US 5854055 Continuation of
Ser. No. US 1989-361944, filed on 5 Jun 1989, now patented, Pat. No. US
5504005 Continuation-in-part of Ser. No. US 1988-223089, filed on 22 Jul
1988, now abandoned Continuation-in-part of Ser. No. US 1988-216390,
filed on 7 Jul 1988, now abandoned Continuation-in-part of Ser. No. US
1988-163546, filed on 3 Mar 1988, now abandoned Continuation-in-part of
Ser. No. US 1987-20451, filed on 2 Mar 1987, now abandoned

DT Utility

FS GRANTED

EXNAM Primary Examiner: McGarry, Sean

LREP Amster, Rothstein & Ebenstein

CLMN Number of Claims: 3

ECL Exemplary Claim: 1

DRWN 26 Drawing Figure(s); 17 Drawing Page(s)

LN.CNT 2158

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 64 OF 194 USPATFULL on STN

AN 2002:24054 USPATFULL

TI Methods of identifying bacterial genes that are incompatible with
bacterial pathogenicity, and the use of such genes, such as cadA, to
reduce pathogenicity in a bacteria or to combat pathogenic bacterial
infections

IN Maurelli, Anthony T., 1429 Winding Waye La., Silver Spring, MD, United
States 20902

Fernandez, Reinaldo E., 3115 Whispering Pines Dr. Apt. #41, Silver
Spring, MD, United States 20906

Bloch, Craig A., 1125 Ferdon Rd., Ann Arbor, MI, United States 48104

Fasano, Alessio, 3128 River Valley Chase, West Friendship, MD, United
States 21794

PI US 6344201 B1 20020205

AI US 1999-281274 19990330 (9)

PRAI US 1998-80202P 19980331 (60)

DT Utility

FS GRANTED

EXNAM Primary Examiner: Graser, Jennifer E.

LREP Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.

CLMN Number of Claims: 3

ECL Exemplary Claim: 1

DRWN 5 Drawing Figure(s); 4 Drawing Page(s)

LN.CNT 1576

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 65 OF 194 USPATFULL on STN

AN 2002:19054 USPATFULL

TI Identification of genes

IN Holden, David William, London, UNITED KINGDOM

Shea, Jacqueline Elizabeth, High Wycombe, UNITED KINGDOM

Hensel, Michael, Munchen, GERMANY, FEDERAL REPUBLIC OF

PA Imperial College Innovations Limited, London, UNITED KINGDOM (non-U.S.
corporation)

Microscience Limited, Berkshire, UNITED KINGDOM (non-U.S. corporation)

PI US 6342215 B1 20020129

AI US 1998-201945 19981201 (9)

RLI Continuation of Ser. No. US 637759, now patented, Pat. No. US 5876931

PRAI GB 1994-24921 19941209
GB 1995-1881 19950131
GB 1995-9239 19950505

DT Utility

FS GRANTED

EXNAM Primary Examiner: Schwartzman, Robert A.

LREP Holland & Knight LLP

CLMN Number of Claims: 21

ECL Exemplary Claim: 1

DRWN 119 Drawing Figure(s); 112 Drawing Page(s)

LN.CNT 7399

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 66 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2002:558905 SCISEARCH

GA The Genuine Article (R) Number: 567GZ

TI Polynucleotide phosphorylase is a global regulator of virulence and
persistence in *Salmonella enterica*

AU Clements M O; Eriksson S; Thompson A; Lucchini S; Hinton J C D; Normark S;
Rhen M (Reprint)

CS Karolinska Inst, Ctr Microbiol & Tumor Biol, Nobels Vag 16, S-17177
Stockholm, Sweden (Reprint); Karolinska Inst, Ctr Microbiol & Tumor Biol,
S-17177 Stockholm, Sweden; Univ Coll London, Wolfson Inst Biomed Res,
London WC1E 6BT, England; AFRC, Inst Food Res, Mol Microbiol Grp, Norwich
NR4 7UA, Norfolk, England; Swedish Inst Infect Dis Control, S-17182 Solna,
Sweden

CYA Sweden; England

SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (25 JUN 2002) Vol. 99, No. 13, pp. 8784-8789.

Publisher: NATL ACAD SCIENCES, 2101 CONSTITUTION AVE NW, WASHINGTON, DC
20418 USA.

ISSN: 0027-8424.

DT Article; Journal

LA English

REC Reference Count: 49

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 67 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2002:554535 CAPLUS

DN 137:245731

TI Disruption of the gene homologous to mammalian Nramp1 in *Mycobacterium*
tuberculosis does not affect virulence in mice

AU Boechat, Neio; Lagier-Roger, Beatrice; Petit, Stephanie; Bordat, Yann;
Rauzier, Jean; Hance, Allan J.; Gicquel, Brigitte; Reyat, Jean-Marc

CS Unite de Genetique Mycobacterienne, Institut Pasteur, Faculte de Medecine
Xavier Bichat, Hopital Bichat-Claude Bernard, INSERM U552, Paris, 75724,
Fr.

SO Infection and Immunity (2002), 70(8), 4124-4131

CODEN: INFIBR; ISSN: 0019-9567

PB American Society for Microbiology

DT Journal

LA English

RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 68 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2003:61495 SCISEARCH

GA The Genuine Article (R) Number: 629DR

TI Involvement of the fadD33 gene in the growth of *Mycobacterium*
tuberculosis in the liver of BALB/c mice

AU Rindi L; Fattorini L; Bonanni D; Iona E; Freer G; Tan D J; Deho G; Orefici

G; Garzelli C (Reprint)

CS Univ Pisa, Dipartimento Patol Sperimentale Biotecnol Med Inf, I-56127
Pisa, Italy (Reprint); Ist Super Sanita, Lab Batteriol & Micol Med,
I-00161 Rome, Italy; Univ Milan, Dipartimento Genet & Biol Microorganismi,
Milan, Italy

CYA Italy

SO MICROBIOLOGY-SGM, (DEC 2002) Vol. 148, Part 12, pp. 3873-3880.

Publisher: SOC GENERAL MICROBIOLOGY, MARLBOROUGH HOUSE, BASINGSTOKE RD,
SPENCERS WOODS, READING RG7 1AG, BERKS, ENGLAND.

ISSN: 1350-0872.

DT Article; Journal

LA English

REC Reference Count: 37

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 69 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2002:530465 SCISEARCH

GA The Genuine Article (R) Number: 564ET

TI Mycobacterium avium genes expressed during growth in human macrophages
detected by selective capture of transcribed sequences (SCOTS)

AU Hou J Y; Graham J E; Clark-Curtiss J E (Reprint)

CS Washington Univ, Dept Biol, Campus Box 1137, St Louis, MO 63130 USA

(Reprint); Washington Univ, Dept Biol, St Louis, MO 63130 USA; Washington
Univ, Dept Mol Microbiol, St Louis, MO 63130 USA

CYA USA

SO INFECTION AND IMMUNITY, (JUL 2002) Vol. 70, No. 7, pp. 3714-3726.

Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904
USA.

ISSN: 0019-9567.

DT Article; Journal

LA English

REC Reference Count: 46

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 70 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2002:818550 CAPLUS

DN 138:118171

TI Characterization of a Mycobacterium ***tuberculosis*** H37Rv
transposon library reveals insertions in 351 ORFs and mutants with altered
virulence

AU McAdam, Ruth A.; Quan, Selwyn; Smith, Debbie A.; Bardarov, Stoyan; Betts,
Joanna C.; Cook, Fiona C.; Hooker, Elizabeth U.; Lewis, Alan P.; Woollard,
Peter; Everett, Martin J.; Lukey, Pauline T.; Bancroft, Gregory J.;
Jacobs, William R., Jr.; Duncan, Ken

CS GlaxoSmithKline, Medicines Research Centre, Stevenage, SG1 2NY, UK

SO Microbiology (Reading, United Kingdom) (2002), 148(10), 2975-2986

CODEN: MROBEO; ISSN: 1350-0872

PB Society for General Microbiology

DT Journal

LA English

RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 71 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2002:359057 SCISEARCH

GA The Genuine Article (R) Number: 543NH

TI Transient requirement of the PrrA-PrrB two-component system for early
intracellular multiplication of Mycobacterium ***tuberculosis***

AU Ewann F; Jackson M; Pethe K; Cooper A; Mielcarek N; Ensergueix D; Gicquel
B; Loch C (Reprint); Supply P

CS Inst Pasteur, INSERM, Lab Mecanismes Mol Pathogenese Bacterienne, U447, 1

Rue Prof Calmette, F-59019 Lille, France (Reprint); Inst Pasteur, INSERM,
Lab Mecanismes Mol Pathogenese Bacterienne, U447, F-59019 Lille, France;
Inst Pasteur, Unit Genet Mycobacterienne, F-75724 Paris, France; Colorado
State Univ, Dept Microbiol, Ft Collins, CO 80523 USA

CYA France; USA

SO INFECTION AND IMMUNITY, (MAY 2002) Vol. 70, No. 5, pp. 2256-2263.

Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904
USA.

ISSN: 0019-9567.

DT Article; Journal

LA English

REC Reference Count: 30

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 72 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2002:127738 SCISEARCH

GA The Genuine Article (R) Number: 518VJ

TI Chromosomal locus that affects pathogenicity of *Rhodococcus fascians*

AU Vereecke D; Cornelis K; Temmerman W; Jaziri M; Van Montagu M; Holsters M
(Reprint); Goethals K

CS State Univ Ghent, Vakgrp Mol Genet, Dept Plantengenet, Vlaams Interuniv

Inst Biotechnol, KL Ledeganckstr 35, B-9000 Ghent, Belgium (Reprint);

State Univ Ghent, Vakgrp Mol Genet, Dept Plantengenet, Vlaams Interuniv

Inst Biotechnol, B-9000 Ghent, Belgium; Free Univ Brussels, Lab Biotechnol

Vegetale, B-1160 Brussels, Belgium

CYA Belgium

SO JOURNAL OF BACTERIOLOGY, (FEB 2002) Vol. 184, No. 4, pp. 1112-1120.

Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904
USA.

ISSN: 0021-9193.

DT Article; Journal

LA English

REC Reference Count: 59

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 73 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 3

AN 2002:738989 CAPLUS

DN 138:330985

TI Prospects for development of new antituberculous drugs

AU Tomioka, Haruaki

CS Japan

SO Kekkaku (2002), 77(8), 573-584

CODEN: KEKKAG; ISSN: 0022-9776

PB Nippon Kekkakubyo Gakkai

DT Journal; General Review

LA Japanese

L4 ANSWER 74 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2003:18872 BIOSIS

DN PREV200300018872

TI Molecular basis of bacterial virulence and survival within infected hosts
and the environment.

AU Raupach, Baerbel (1); Reyrat, Jean-Marc

CS (1) Dept of Cellular Microbiology, Max Planck Institut fuer

Infektionsbiologie, Schumannstrasse 21/22, Berlin, D-10117, Germany:

jmreyrat@pasteur.fr Germany

SO Trends in Microbiology, (December 2002, 2002) Vol. 10, No. 12, pp.
547-550. print.

Meeting Info.: Molecular Basis of Bacterial Virulence and Survival within
Infected Hosts and in the Environment. Spetsai, Greece September 03-13,
2002

ISSN: 0966-842X.

DT Conference

LA English

L4 ANSWER 75 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:609024 BIOSIS

DN PREV200200609024

TI Identification of proteins expressed by Mycobacterium avium under trace element concentration found within the macrophage phagosome.

AU Li, Y. (1); Wagner, D. (1); Wu, M. (1); Bermudez, L. E. (1)

CS (1) Kuzell Institute, San Francisco, CA USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 486. <http://www.asmta.org/mtgsrc/generalmeeting.htm>. print.

Meeting Info.: 102nd General Meeting of the American Society for Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for Microbiology

. ISSN: 1060-2011.

DT Conference

LA English

L4 ANSWER 76 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:609000 BIOSIS

DN PREV200200609000

TI Analysis of the eis promoter of Mycobacterium ***tuberculosis*** using transcriptional fusions to gfp and flow cytometry.

AU Roberts, E. A. (1); Friedman, R. L. (1)

CS (1) University of Arizona, Tucson, AZ USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 481. <http://www.asmta.org/mtgsrc/generalmeeting.htm>. print.

Meeting Info.: 102nd General Meeting of the American Society for Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for Microbiology

. ISSN: 1060-2011.

DT Conference

LA English

L4 ANSWER 77 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2003:328470 BIOSIS

DN PREV200300328470

TI Mycobacterial: Host cell interactions.

AU Bermudez, Luiz E. (1)

CS (1) Kuzell Inst., San Francisco, CA, USA USA

SO Abstracts of the Interscience Conference on Antimicrobial Agents and Chemotherapy, (2002) Vol. 42, pp. 463. print.

Meeting Info.: 42nd Interscience Conference on Antimicrobial Agents and Chemotherapy San Diego, CA, USA September 27-30, 2002 American Society for Microbiology

DT Conference

LA English

L4 ANSWER 78 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2002:618180 SCISEARCH

GA The Genuine Article (R) Number: 574UC

TI Never say never again: protein glycosylation in pathogenic bacteria

AU Benz I; Schmidt M A (Reprint)

CS Univ Klinikum Munster, Zentrum Mol Biol Entzündung, Inst Infektiol, Munster, Germany (Reprint)

CYA Germany

SO MOLECULAR MICROBIOLOGY, (JUL 2002) Vol. 45, No. 2, pp. 267-276.

Publisher: BLACKWELL PUBLISHING LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 ONE, OXON, ENGLAND.

ISSN: 0950-382X.

DT General Review; Journal

LA English

REC Reference Count: 65

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 79 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2002:954467 CAPLUS

DN 138:298390

TI Development of a mycobacterial gene knock-out system using sequence-specific recombinase FLP/FRT and its application to the construction of a rhamnose biosynthetic gene rmlD deletion mutant

AU Lee, Kwang-Chul; Lee, Jong-Seok; Lee, Sang-Ji; Lee, Kwan-Ho; Lee, Tae-Jin; Shin, Hyun-Jung; Choi, Ji-Eun; Park, Ho-Sun; Kim, Sung-Kwang; Lee, Tae-Yoon

CS Departments of Microbiology and Internal Medicine, College of Medicine, Yeungnam University, Namku, Daegu, 705-717, S. Korea

SO Journal of Bacteriology and Virology (2002), 32(3), 221-230

CODEN: JBVOAH; ISSN: 1598-2467

PB Journal of Bacteriology and Virology

DT Journal

LA Korean

L4 ANSWER 80 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2003:134496 SCISEARCH

GA The Genuine Article (R) Number: BW02K

TI High throughput in vivo screens: Signature-tagged mutagenesis

AU West N (Reprint); Sansonetti P; Tang C M

CS Univ London Imperial Coll Sci Technol & Med, Ctr Mol Microbiol & Infect, Flowers Bldg, Armstrong Rd, London SW7 2AZ, England (Reprint); Univ London Imperial Coll Sci Technol & Med, Ctr Mol Microbiol & Infect, London SW7 2AZ, England; Inst Pasteur, Unite Pathogenie Microbienne Mol, F-75724 Paris 15, France

CYA England; France

SO FUNCTIONAL MICROBIAL GENOMICS, (DEC 2002) Vol. 33, pp. 153-165.

Publisher: ACADEMIC PRESS INC, 525 B STREET, SUITE 1900, SAN DIEGO, CA 92101-4495 USA.

ISSN: 0580-9517.

DT General Review; Journal

LA English

REC Reference Count: 40

L4 ANSWER 81 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

DUPLICATE 4

AN 2002:412642 BIOSIS

DN PREV200200412642

TI Mycobacterium ***tuberculosis*** mammalian cell entry operon (mce) homologs in Mycobacterium other than ***tuberculosis*** (MOTT).

AU Haile, Yoseph; Caugant, Dominique A.; Bjune, Gunnar; Wiker, Harald G. (1)

CS (1) Norwegian Institute of Public Health, Nydalen, N-0403, P.O. Box 4404, Oslo: harald.g.wiker@folkehelsa.no Norway

SO FEMS Immunology and Medical Microbiology, (3 June, 2002) Vol. 33, No. 2, pp. 125-132. <http://www.elsevier.com/locate/femsim>. print.

ISSN: 0928-8244.

DT Article

LA English

L4 ANSWER 82 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:634272 BIOSIS
DN PREV200200634272
TI The genetics of Mycobacterium ***tuberculosis*** virulence.
AU Smith, I. (1); Dubnau, E. (1); Gold, B. (1); Gomez, M. (1); Manganelli, R.
(1); Perez, C. (1); Rodriguez, G. M. (1); Walters, S. (1); Chan, J.
CS (1) Public Health Research Institute, New York, NY USA
SO Tuberculosis (Edinburgh), (2002) Vol. 82, No. 2-3, pp. 124. print.
Meeting Info.: 36th Annual Research Conference of the US-Japan Cooperative
Medical Science Program Tuberculosis and Leprosy Panel Louisiana, USA July
15-17, 2001
ISSN: 1472-9792.
DT Conference
LA English

L4 ANSWER 83 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2003:28087 SCISEARCH
GA The Genuine Article (R) Number: BV73G
TI Microbial gene expression elucidated by selective capture of transcribed
sequences (SCOTS)
AU Daigle F (Reprint); Hou J Y; Clark-Curtiss J E
CS Univ Montreal, Dept Microbiol, Montreal, PQ H3C 3J7, Canada (Reprint);
Washington Univ, Dept Biol, St Louis, MO 63130 USA; Washington Univ, Dept
Mol Microbiol, St Louis, MO 63130 USA
CYA Canada; USA
SO BACTERIAL PATHOGENESIS, PT C, (16 DEC 2002) Vol. 358, pp. 108-122.
Publisher: ACADEMIC PRESS INC, 525 B STREET, SUITE 1900, SAN DIEGO, CA
92101-4495 USA.
ISSN: 0076-6879.
DT General Review; Journal
LA English
REC Reference Count: 32

L4 ANSWER 84 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:585007 BIOSIS
DN PREV200200585007
TI Identification and characterization of Enterococcus faecalis
metal-dependent repressor, EfaR with homology to the DtxR.
AU Bergeron, L. J. (1); Andrew, T. (1); Murphy, J. R.; Bishai, W. R.;
Harrison, R. J. (1)
CS (1) Advanced Microbial Solutions Corp, Cambridge, MA USA
SO Abstracts of the General Meeting of the American Society for Microbiology,
(2002) Vol. 102, pp. 91. <http://www.asmta.org/mtgsrvc/generalmeeting.htm>.
print.
Meeting Info.: 102nd General Meeting of the American Society for
Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for
Microbiology
. ISSN: 1060-2011.
DT Conference
LA English

L4 ANSWER 85 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:570980 BIOSIS
DN PREV200200570980
TI Identification of a cutinase gene in Mycobacterium marinum linked to
virulence.
AU Ruley, K. M. (1); Trucksis, M. (1)
CS (1) University of Maryland, Baltimore, MD USA
SO Abstracts of the General Meeting of the American Society for Microbiology,
(2002) Vol. 102, pp. 58. <http://www.asmta.org/mtgsrvc/generalmeeting.htm>.
print.
Meeting Info.: 102nd General Meeting of the American Society for

Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for
Microbiology

ISSN: 1060-2011.

DT Conference

LA English

L4 ANSWER 86 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2002:165017 SCISEARCH

GA The Genuine Article (R) Number: 520PV

TI Use of signature-tagged mutagenesis in pathogenesis studies

AU Meccas J (Reprint)

CS Tufts Univ, Sch Med, Dept Mol Biol & Microbiol, 136 Harrison Ave, Boston,

MA 02111 USA (Reprint); Tufts Univ, Sch Med, Dept Mol Biol & Microbiol,

Boston, MA 02111 USA

CYA USA

SO CURRENT OPINION IN MICROBIOLOGY, (FEB 2002) Vol. 5, No. 1, pp. 33-37.

Publisher: CURRENT BIOLOGY LTD, 84 THEOBALDS RD, LONDON WC1X 8RR, ENGLAND.

ISSN: 1369-5274.

DT General Review; Journal

LA English

REC Reference Count: 37

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 87 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2001:380417 CAPLUS

DN 135:484

TI Methods and compositions using SH3-ligand peptides for treatment of
microorganism-mediated disease

IN Murphy, John R.; Harrison, Robert J.

PA Advanced Microbial Solutions Corporation, USA

SO PCT Int. Appl., 54 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 2001035981	A1	20010525	WO 2000-US31721	20001120
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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-166600P P 19991119

OS MARPAT 135:484

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 88 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2001:208420 CAPLUS

DN 134:247979

TI ***Virulence*** ***genes*** of Mycobacterium marinum and M.
tuberculosis, avirulent mutant mycobacteria and attenuated
vaccines

IN Trucksis, Michele

PA University of Maryland, Baltimore, USA; United States Government, as
Represented by Department of Veterans Affairs

SO PCT Int. Appl., 99 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 2001019993	A2	20010322	WO 2000-US25512	20000918
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WO 2001019993	A3	20011122		
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W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-154322P P 19990917

L4 ANSWER 89 OF 194 USPATFULL on STN

AN 2001:165443 USPATFULL

TI Attenuated recombinant mycobacteria useful as immunogens or as vaccine
components

IN Gicquel, Brigitte, Paris, France

Guilhot, Christophe, Issy Les Moulineaux, France

Jackson, Mary, Paris, France

PA Institut Pasteur (non-U.S. corporation)

PI US 2001024653 A1 20010927

AI US 2001-851951 A1 20010509 (9)

RLI Division of Ser. No. US 1998-95801, filed on 11 Jun 1998, GRANTED, Pat.
No. US 6261568

PRAI US 1997-49390P 19970611 (60)

DT Utility

FS APPLICATION

LREP FINNEGAN, HENDERSON, FARABOW, GARRETT &, DUNNER LLP, 1300 I STREET, NW,
WASHINGTON, DC, 20005

CLMN Number of Claims: 32

ECL Exemplary Claim: 1

DRWN 11 Drawing Page(s)

LN.CNT 1652

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 90 OF 194 USPATFULL on STN

AN 2001:150270 USPATFULL

TI DNA molecule fragments encoding for cellular uptake of mycobacterium
tuberculosis and uses thereof

IN Riley, Lee W., New York, NY, United States

Chong, Pele, Richmond Hill, Canada

PI US 2001019716 A1 20010906

AI US 2001-754153 A1 20010104 (9)

RLI Continuation of Ser. No. US 1996-689411, filed on 7 Aug 1996, GRANTED,
Pat. No. US 6224881

DT Utility

FS APPLICATION

LREP Michael L. Goldman, Esq., NIXON PEABODY LLP, Clinton Square, P. O. Box
31051, Rochester, NY, 14603

CLMN Number of Claims: 52

ECL Exemplary Claim: 1

DRWN 7 Drawing Page(s)

LN.CNT 1958

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 91 OF 194 USPATFULL on STN
AN 2001:214842 USPATFULL
TI Abundant, well distributed and hyperpolymorphic simple sequence repeats
in prokaryote genomes and use of same for prokaryote classification and
typing
IN Kashi, Yechezkel, Haifa, Israel
Gur-Arie, Riva, Binyamina, Israel
Cohen, Cyril, Nebher, Israel
Eitan, Yuval, Jerusalem, Israel
Shelef, Leora, Bloomfield Vill., MI, United States
Hallerman, Eric, Blacksburg, VA, United States
PA Technion Research and Development Foundation Ltd., Haifa, Israel
(non-U.S. corporation)
PI US 6322985 B1 20011127
AI US 1999-472035 19991227 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Fredman, Jeffrey
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 8 Drawing Page(s)
LN.CNT 1708
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 92 OF 194 USPATFULL on STN
AN 2001:190895 USPATFULL
TI Identification of virulence determinants activators in prokaryotic
pathogens
IN Murphy, John R., Boston, MA, United States
Sun, Li, Oxford, United Kingdom
PA Boston Medical Center Corporation, Boston, MA, United States (U.S.
corporation)
PI US 6309817 B1 20011030
AI US 1999-408618 19990930 (9)
PRAI US 1998-102545P 19980930 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Stucker, Jeffrey; Assistant Examiner: Winkler, Ulrike
LREP Lerner, David, Littenberg, Krumholz & Mentlik, LLP
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 1310
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 93 OF 194 USPATFULL on STN
AN 2001:157804 USPATFULL
TI Dim mutants of mycobacteria and use thereof
IN Cox, Jeffery S., Larchmont, NY, United States
Jacobs, Jr., William R., City Island, NY, United States
PA Albert Einstein College of Medicine of Yeshiva University, Bronx, NY,
United States (U.S. corporation)
PI US 6290966 B1 20010918
AI US 1999-350326 19990709 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Swart, Rodney P.
LREP Amster, Rothstein & Ebenstein
CLMN Number of Claims: 16

ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 588
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 94 OF 194 USPATFULL on STN
AN 2001:126120 USPATFULL
TI Tissue-specific and pathogen-specific toxic agents and ribozymes
IN Norris, James, Mt. Pleasant, SC, United States
Clawson, Gary, Bethesda, MD, United States
Westwater, Caroline, Mt. Pleasant, SC, United States
Schofield, David, Mt. Pleasant, SC, United States
Schmidt, Michael, Mt. Pleasant, SC, United States
Hoel, Brian, Charleston, SC, United States
Dolan, Joseph, Mt. Pleasant, SC, United States
Pan, Wei-Hua, Hummelstown, PA, United States
PA MUSC Foundation for Research Development, Charleston, SC, United States
(U.S. corporation)
The Penn State Research Foundation, University Park, PA, United States
(U.S. corporation)
PI US 6271359 B1 20010807
AI US 1999-291902 19990414 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Yucel, Remy; Assistant Examiner: Schmidt, M
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 8
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 2816
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 95 OF 194 USPATFULL on STN
AN 2001:125562 USPATFULL
TI Recombinant mycobacterial vaccine
IN Bloom, Barry R., Hastings on Hudson, NY, United States
Davis, Ronald W., Palo Alto, CA, United States
Jacobs, Jr., William R., Bronx, NY, United States
Young, Richard A., Winchester, MA, United States
Husson, Robert N., Takoma Park, MD, United States
PA Albert Einstein College of Medicine of Yeshiva University, Bronx, NY,
United States (U.S. corporation)
The Board of Trustees of the Leland Stanford, Jr. University, Palo Alto,
CA, United States (U.S. corporation)
Whitehead Institute for Biomedical Research, Cambridge, MA, United
States (U.S. corporation)
PI US 6270776 B1 20010807
AI US 1995-454075 19950530 (8)
RLI Division of Ser. No. US 1989-361944, filed on 5 Jun 1989, now patented,
Pat. No. US 5504005 Continuation-in-part of Ser. No. US 1988-223089,
filed on 22 Jul 1988, now abandoned Continuation-in-part of Ser. No. US
1988-216390, filed on 7 Jul 1988, now abandoned Continuation-in-part of
Ser. No. US 1988-163546, filed on 3 Mar 1988, now abandoned
Continuation-in-part of Ser. No. US 1987-20451, filed on 2 Mar 1987, now
abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: McGarry, Sean
LREP Hamilton, Brook, Smith & Reynolds, P.C.
CLMN Number of Claims: 29
ECL Exemplary Claim: 1

DRWN 23 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 2263
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 96 OF 194 USPATFULL on STN
AN 2001:111839 USPATFULL
TI Attenuated recombinant mycobacteria useful as immunogens or as vaccine components
IN Gicquel, Brigitte, Paris, France
Guilhot, Christophe, Issy les Moulineaux, France
Jackson, Mary, Paris, France
PA Institut Pasteur, Paris, France (non-U.S. corporation)
PI US 6261568 B1 20010717
AI US 1998-95801 19980611 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Swart, Rodney P.
LREP Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
CLMN Number of Claims: 3
ECL Exemplary Claim: 1
DRWN 22 Drawing Figure(s); 11 Drawing Page(s)
LN.CNT 1595
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 97 OF 194 USPATFULL on STN
AN 2001:111832 USPATFULL
TI Method of stimulating an immune response by administration of host organisms that express intimin alone or as a fusion protein with one or more other antigens
IN Stewart, Jr., C. Neal, Greensboro, NC, United States
McKee, Marian L., Great Falls, VA, United States
O'Brien, Alison D., Bethesda, MD, United States
Wachtel, Marian R., Albany, CA, United States
PA Henry M. Jackson Foundation for the Advancement of Military Medicine, Rockville, MD, United States (U.S. corporation)
PI US 6261561 B1 20010717
AI US 1997-840466 19970418 (8)
PRAI US 1996-15657P 19960419 (60)
US 1996-15938P 19960422 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Smith, Lynette R F.; Assistant Examiner: Portner, Ginny Allen
LREP Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 23 Drawing Page(s)
LN.CNT 2817
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 98 OF 194 USPATFULL on STN
AN 2001:86205 USPATFULL
TI Target system
IN Emi, Bernhard, Kaenelgasse 17, Zollikofen, Switzerland 3052
PI US 6245502 B1 20010612
AI US 1998-26904 19980219 (9)
PRAI EP 1997-102616 19970219
DT Utility
FS GRANTED
EXNAM Primary Examiner: Borin, Michael
CLMN Number of Claims: 8

ECL Exemplary Claim: 1
DRWN 5 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1138
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 99 OF 194 USPATFULL on STN
AN 2001:63259 USPATFULL
TI DNA molecule fragments encoding for cellular uptake of Mycobacterium
tuberculosis and uses thereof
IN Riley, Lee W., New York, NY, United States
Chong, Pele, Richmond Hill, Canada
PA Cornell Research Foundation, Inc., Ithaca, NY, United States (U.S.
corporation)
Connaught Laboratories Limited, Canada (non-U.S. corporation)
PI US 6224881 B1 20010501
AI US 1996-689411 19960807 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Swart, Rodney P.
LREP Nixon Peabody LLP
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 13 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 1606
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 100 OF 194 USPATFULL on STN
AN 2001:51779 USPATFULL
TI Method compositions and kit for detection
IN Leushner, James, North York, Canada
Hui, May, Toronto, Canada
Dunn, James M., Scarborough, Canada
LaCroix, Jean-Michel, Etobicoke, Canada
PA Visible Genetics Inc., Toronto, Canada (non-U.S. corporation)
PI US 6214555 B1 20010410
AI US 1999-311260 19990513 (9)
RLI Continuation-in-part of Ser. No. US 1998-9483, filed on 20 Jan 1998
Continuation-in-part of Ser. No. US 1996-640672, filed on 1 May 1996,
now patented, Pat. No. US 5789168 Continuation-in-part of Ser. No. US
1996-684498, filed on 19 Jul 1996, now patented, Pat. No. US 5830657
Continuation-in-part of Ser. No. US 1997-807138, filed on 22 Feb 1997,
now patented, Pat. No. US 5888736
DT Utility
FS Granted
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Oppedahl & Larson LLP
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 903
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 101 OF 194 USPATFULL on STN
AN 2001:51767 USPATFULL
TI DNA molecule encoding for cellular uptake of Mycobacterium
tuberculosis and uses thereof
IN Riley, Lee W., New York, NY, United States
PA Cornell Research Foundation, Inc., Ithaca, NY, United States (U.S.
corporation)
PI US 6214543 B1 20010410
AI US 1995-461002 19950605 (8)

RLI Division of Ser. No. US 1995-392210, filed on 22 Feb 1995
Continuation-in-part of Ser. No. US 1993-118442, filed on 2 Sep 1993
DT Utility
FS Granted
EXNAM Primary Examiner: Swart, Rodney P.
LREP Nixon Peabody LLP
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 9 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 1323
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 102 OF 194 USPATFULL on STN
AN 2001:25424 USPATFULL
TI Vectors for the diagnosis and treatment of solid tumors including melanoma
IN Pawelek, John M., Hamden, CT, United States
Bermudes, David, Wallingford, CT, United States
Low, Kenneth Brooks, Guilford, CT, United States
PA Yale University, New Haven, CT, United States (U.S. corporation)
PI US 6190657 B1 20010220
AI US 1996-658034 19960604 (8)
RLI Continuation-in-part of Ser. No. US 1995-486422, filed on 7 Jun 1995, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Sandals, William
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 66
ECL Exemplary Claim: 1
DRWN 45 Drawing Figure(s); 38 Drawing Page(s)
LN.CNT 4716
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 103 OF 194 USPATFULL on STN
AN 2001:10548 USPATFULL
TI DNA molecule conferring on Mycobacterium ***tuberculosis*** resistance against antimicrobial reactive oxygen and nitrogen intermediates
IN Riley, Lee W., Berkeley, CA, United States
Nathan, Carl F., Larchmont, NY, United States
Ehrt, Sabine, Berkeley, CA, United States
PA Cornell Research Foundation, Inc., Ithaca, NY, United States (U.S. corporation)
PI US 6177086 B1 20010123
AI US 1998-67626 19980428 (9)
PRAI US 1997-45688P 19970506 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Swart, Rodney P.
LREP Nixon Peabody LLP
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 1844
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 104 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2001:943887 SCISEARCH
GA The Genuine Article (R) Number: 494QP
TI Application of high-density array-based signature-tagged mutagenesis to

discover novel Yersinia virulence-associated genes

AU Karlyshev A V; Oyston P C F; Williams K; Clark G C; Titball R W; Winzeler E A; Wren B W (Reprint)

CS Univ London London Sch Hyg & Trop Med, Dept Infect & Trop Dis, Keppel St, London WC1E 7HT, England (Reprint); Univ London London Sch Hyg & Trop Med, Dept Infect Dis, London WC1E 7HT, England; Def Sci & Technol Lab, CBS Porton Down, Salisbury SP4 0JQ, Wilts, England; Stanford Univ, Sch Med, Dept Biochem, Stanford, CA 94305 USA

CYA England; USA

SO INFECTION AND IMMUNITY, (DEC 2001) Vol. 69, No. 12, pp. 7810-7819.

Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.

ISSN: 0019-9567.

DT Article; Journal

LA English

REC Reference Count: 56

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 105 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 5

AN 2002:52251 CAPLUS

DN 137:1010

TI Identification of bacterial genes required for in-vivo survival

AU Tang, C. M.; Bakshi, S.; Sun, Y.-H.

CS University Department of Paediatrics, John Radcliffe Hospital, Oxford, OX3 9DU, UK

SO Journal of Pharmacy and Pharmacology (2001), 53(12), 1575-1579

CODEN: JPPMAB; ISSN: 0022-3573

PB Pharmaceutical Press

DT Journal; General Review

LA English

RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE.FORMAT

L4 ANSWER 106 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2001:418127 CAPLUS

DN 136:97176

TI Regulation of catalase-peroxidase (KatG) expression, isoniazid sensitivity and virulence by FurA of Mycobacterium ***tuberculosis***

AU Pym, Alexander S.; Domenech, Pilar; Honore, Nadine; Song, Jian; Deretic, Vojo; Cole, Stewart T.

CS Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, Paris, 75724, Fr.

SO Molecular Microbiology (2001), 40(4), 879-889

CODEN: MOMIEE; ISSN: 0950-382X

PB Blackwell Science Ltd.

DT Journal

LA English

RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE.FORMAT

L4 ANSWER 107 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2001:810024 SCISEARCH

GA The Genuine Article (R) Number: 478BK

TI Understanding the physiology of difficult, pathogenic bacteria from analysis of their genome sequences

AU Wheeler P R (Reprint)

CS Vet Labs Agcy, Dept Bacterial Dis, TB Res Unit, Weybridge KT15 3NB, Surrey, England (Reprint)

CYA England

SO JOURNAL OF MEDICAL MICROBIOLOGY, (OCT 2001) Vol. 50, No. 10, pp. 843-846.

Publisher: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST, PHILADELPHIA, PA

19106-3621 USA.
ISSN: 0022-2615.
DT Editorial; Journal
LA English
REC Reference Count: 25

L4 ANSWER 108 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:251695 BIOSIS
DN PREV200200251695
TI Construction of epitope-tagging transposons for analysis of Mycobacterium
tuberculosis
AU Chiang, S. L. (1); Rubin, E. J. (1)
CS (1) Harvard School of Public Health, Boston, MA USA
SO Abstracts of the General Meeting of the American Society for Microbiology,
(2001) Vol. 101, pp. 714. <http://www.asmta.org/mtgsrc/generalmeeting.htm>.
print.
Meeting Info.: 101st General Meeting of the American Society for
Microbiology Orlando, FL, USA May 20-24, 2001
ISSN: 1060-2011.
DT Conference
LA English

L4 ANSWER 109 OF 194 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS
RESERVED. on STN
AN 2001403773 EMBASE
TI Microarray analysis of pathogens and their interaction with hosts.
AU Kato-Maeda M.; Gao Q.; Small P.M.
CS P.M. Small, Div. of Infect. Dis./Geographic Med., Department of Medicine,
Stanford University Medical School, 300 Pasteur Drive, Stanford, CA 94305,
United States. peter@molepi.stanford.edu
SO Cellular Microbiology, (2001) 3/11 (713-719).
Refs: 34
ISSN: 1462-5814 CODEN: CEMIF5
CY United Kingdom
DT Journal; General Review
FS 004 Microbiology
005 General Pathology and Pathological Anatomy
006 Internal Medicine
037 Drug Literature Index
038 Adverse Reactions Titles
LA English
SL English

L4 ANSWER 110 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:792976 CAPLUS
DN 136:82578
TI Mycobacterium smegmatis: an absurd model for ***tuberculosis*** ?
comments
AU Reyrat, Jean-Marc; Kahn, Daniel
CS Unite de Genetique Mycobacterienne, Institut Pasteur, Paris, 75724, Fr.
SO Trends in Microbiology (2001), 9(10), 472-473
CODEN: TRMIEA; ISSN: 0966-842X
PB Elsevier Science Ltd.
DT Journal
LA English
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 111 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:584683 CAPLUS
DN 136:195200

TI The Mycobacterium ***tuberculosis*** ECF sigma factor :sigma.E: role
in global gene expression and survival in macrophages
AU Manganelli, Riccardo; Voskuil, Martin I.; Schoolnik, Gary K.; Smith, Issar
CS TB Center, The Public Health Research Institute, New York, NY, 10016, USA
SO Molecular Microbiology (2001), 41(2), 423-437
CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell Science Ltd.
DT Journal
LA English
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 112 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 6
AN 2001:605476 CAPLUS
DN 136:180517

TI Genes of Mycobacterium ***tuberculosis*** H37Rv downregulated in the
attenuated strain H37Ra are restricted to M. ***tuberculosis***
complex species
AU Rindi, L.; Lari, N.; Garzelli, C.
CS Dipartimento di Patologia Sperimentale, Biotechnologie Mediche,
Infettivologia ed Epidemiologia, Universita di Pisa, Pisa, I-56127, Italy
SO Microbiologica (2001), 24(3), 289-294
CODEN: MIBLDR; ISSN: 1121-7138
PB Luigi Ponzio e Figlio Editori
DT Journal
LA English
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 113 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2001:778285 SCISEARCH
GA The Genuine Article (R) Number: 476AQ
TI The impact of microbial genomics on antimicrobial drug development
AU Tang C M (Reprint); Moxon E R
CS Univ Oxford, John Radcliffe Hosp, Dept Paediat, Oxford OX3 9DU, England
(Reprint)
CYA England
SO ANNUAL REVIEW OF GENOMICS AND HUMAN GENETICS, (SEP 2001) Vol. 2, pp.
259-269.
Publisher: ANNUAL REVIEWS, 4139 EL CAMINO WAY, PO BOX 10139, PALO ALTO, CA
94303-0139 USA.
ISSN: 1527-8204.
DT General Review; Journal
LA English
REC Reference Count: 39
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 114 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2001:180790 SCISEARCH
GA The Genuine Article (R) Number: 402QJ
TI Applied genome research in the field of human vaccines
AU Berthet F X; Coche T (Reprint); Vinals C
CS SmithKline Beecham Biol, 89 Rue Inst, B-1330 Rixensart, Belgium (Reprint);
SmithKline Beecham Biol, B-1330 Rixensart, Belgium
CYA Belgium
SO JOURNAL OF BIOTECHNOLOGY, (13 FEB 2001) Vol. 85, No. 2, pp. 213-226.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM,
NETHERLANDS.
ISSN: 0168-1656.
DT Article; Journal
LA English

REC Reference Count: 80

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 115 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2001:418135 SCISEARCH

GA The Genuine Article (R) Number: 432VQ

TI Antibacterial vaccine design using genomics and proteomics

AU Grandi G (Reprint)

CS Chiron SpA, Dept Biol Mol, Via Fiorentina 1, I-53100 Siena, Italy
(Reprint); Chiron SpA, Dept Biol Mol, I-53100 Siena, Italy

CYA Italy

SO TRENDS IN BIOTECHNOLOGY, (MAY 2001) Vol. 19, No. 5, pp. 181-188.

Publisher: ELSEVIER SCIENCE LONDON, 84 THEOBALDS RD, LONDON WC1X 8RR,
ENGLAND.

ISSN: 0167-7799.

DT General Review; Journal

LA English

REC Reference Count: 49

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 116 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7

AN 2001:374572 BIOSIS

DN PREV200100374572

TI An essential role for phoP in Mycobacterium ***tuberculosis***
virulence.

AU Perez, Esther; Samper, Sofia; Bordas, Yann; Guilhot, Christophe; Gicquel,
Brigitte; Martin, Carlos (1)

CS (1) Departamento de Microbiologia, Medicina Preventiva y Salud Publica,
Universidad de Zaragoza, C/Domingo Miral sn, 50009, Zaragoza:
carlos@posta.unizar.es Spain

SO Molecular Microbiology, (July, 2001) Vol. 41, No. 1, pp. 179-187. print.
ISSN: 0950-382X.

DT Article

LA English

SL English

L4 ANSWER 117 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8

AN 2001:374178 BIOSIS

DN PREV200100374178

TI Regulation of ***virulence*** ***genes*** in Mycobacterium
tuberculosis .

AU Mehrotra, Jyoti; Bishai, William R. (1)

CS (1) Center for Tuberculosis Research, Johns Hopkins School of Hygiene and
Public Health, 615 N. Wolfe Street, Baltimore, MD, 21205:
wbishai@jhsp.edu USA

SO IJMM International Journal of Medical Microbiology, (May, 2001) Vol. 291,
No. 2, pp. 171-182. print.
ISSN: 1438-4221.

DT General Review

LA English

SL English

L4 ANSWER 118 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9

AN 2001:484285 BIOSIS

DN PREV200100484285

TI Disease model: Pulmonary ***tuberculosis*** .

AU McMurray, David N. (1)

CS (1) Dept of Medical Microbiology and Immunology, Texas A and M University

System Health Science Center, Reynolds Medical Building, College Station,
TX, 77843-1114: dmcmurray@tamu.edu USA
SO Trends in Molecular Medicine, (March, 2001) Vol. 7, No. 3, pp. 135-137.
print.
ISSN: 1471-4914.
DT General Review
LA English
SL English

L4 ANSWER 119 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10
AN 2001:399393 BIOSIS
DN PREV200100399393
TI Virulence factors of Mycobacterium bovis.
AU Collins, D. M. (1)
CS (1) Wallaceville Animal Research Centre, AgResearch, Upper Hutt:
desmond.collins@agresearch.co.nz New Zealand
SO Tuberculosis (Edinburgh), (2001) Vol. 81, No. 1-2, pp. 97-102. print.
ISSN: 1472-9792.
DT Article
LA English
SL English

L4 ANSWER 120 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2001:176573 SCISEARCH
GA The Genuine Article (R) Number: 403PK
TI Recent advances in large-scale transposon mutagenesis
AU Hamer L; DeZwaan T M; Montenegro-Chamorro M V; Frank S A; Hamer J E
(Reprint)
CS Paradigm Genet Inc, 104 Alexander Dr, Bldg 2, Res Triangle Pk, NC 27709
USA (Reprint); Paradigm Genet Inc, Res Triangle Pk, NC 27709 USA
CYA USA
SO CURRENT OPINION IN CHEMICAL BIOLOGY, (FEB 2001) Vol. 5, No. 1, pp. 67-73.
Publisher: CURRENT BIOLOGY LTD, 84 THEOBALDS RD, LONDON WC1X 8RR, ENGLAND.
ISSN: 1367-5931.
DT General Review; Journal
LA English
REC Reference Count: 53
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 121 OF 194 USPATFULL on STN
AN 2000:98234 USPATFULL
TI Method of selection of allelic exchange mutants
IN Pelicic, Vladimir, Paris, France
Reyrat, Jean-Marc, Paris, France
Gicquel, Brigitte, Paris, France
Guilhot, Christophe, Issy les Moulineaux, France
Jackson, Mary, Paris, France
PA Institut Pasteur, Paris, France (non-U.S. corporation)
PI US 6096549 20000801
AI US 1997-872917 19970611 (8)
RLI Continuation-in-part of Ser. No. US 1996-661658, filed on 11 Jun 1996,
now patented, Pat. No. US 5843664
DT Utility
FS Granted
EXNAM Primary Examiner: Schwartzman, Robert A.
LREP Finnegan, Henderson, Farabow, Gattett & Dunner, L.L.P.
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN 15 Drawing Figure(s); 15 Drawing Page(s)
LN.CNT 1360

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 122 OF 194 USPATFULL on STN
AN 2000:70976 USPATFULL
TI DNA molecule encoding for cellular uptake of Mycobacterium
tuberculosis and uses thereof
IN Riley, Lee W., Berkeley, CA, United States
PA Cornell Research Foundation, Inc., Ithaca, NY, United States (U.S.
corporation)
PI US 6072048 20000606
AI US 1997-907229 19970806 (8)
PRAI US 1997-40097P 19970310 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Swartz, Rodney P.
LREP Nixon Peabody LLP
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 1305

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 123 OF 194 USPATFULL on STN
AN 2000:18049 USPATFULL
TI Recombinant avirulent immunogenic S typhi having rpos positive phenotype
IN Curtiss, III, Roy, St. Louis, MO, United States
Nickerson, Cheryl A., Chesterfield, MO, United States
PA Washington University, St. Louis, MO, United States (U.S. corporation)
PI US 6024961 20000215
AI US 1997-970789 19971114 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Mosher, Mary E.
LREP Howell & Haferkamp, L.C.
CLMN Number of Claims: 41
ECL Exemplary Claim: 1,39
DRWN 10 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 2837

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 124 OF 194 USPATFULL on STN
AN 2000:12617 USPATFULL
TI H. influenzae HxuB and HxuC genes, proteins and methods of use
IN Hansen, Eric J., Plano, TX, United States
Cope, Leslie D., Mesquite, TX, United States
Jarosik, Gregory P., Arlington, TX, United States
Hanson, Mark S., Columbia, MD, United States
PA Board of Regents, The University of Texas System, Austin, TX, United
States (U.S. corporation)
PI US 6020154 20000201
AI US 1995-425843 19950420 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Wax, Robert A.; Assistant Examiner: Srivastava, Devesh
LREP Arnold, White & Durkee
CLMN Number of Claims: 77
ECL Exemplary Claim: 20
DRWN 7 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 4068

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 125 OF 194 USPATFULL on STN
AN 2000:7170 USPATFULL
TI Identification of genes
IN Holden, David William, London, United Kingdom
PA Imperial College Innovations Limited, London, United Kingdom (non-U.S. corporation)
PI US 6015669 20000118
AI US 1997-871355 19970609 (8)
RLI Continuation of Ser. No. WO 1995-GB2875, filed on 11 Dec 1995
PRAI GB 1994-24921 19941209
GB 1995-1881 19950131
GB 1995-9239 19950505
WO 1995-GB2875 19951211
DT Utility
FS Granted
EXNAM Primary Examiner: Marschel, Ardin H.; Assistant Examiner: Whisenant, Ethan
LREP Arnall Golden & Gregory, LLP
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 116 Drawing Figure(s); 112 Drawing Page(s)
LN.CNT 7898
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 126 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 11
AN 2000:439757 BIOSIS
DN PREV200000439757
TI Cloning and characterization of secretory tyrosine phosphatases of Mycobacterium ***tuberculosis***
AU Koul, Anil; Choidas, Axel; Treder, Martin; Tyagi, Anil K.; Drlca, Karl; Singh, Yogendra; Ullrich, Axel (1)
CS (1) Department of Molecular Biology, Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18A, 82152, Martinsried Germany
SO Journal of Bacteriology, (October, 2000) Vol. 182, No. 19, pp. 5425-5432. print.
ISSN: 0021-9193.
DT Article
LA English
SL English

L4 ANSWER 127 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 2000:470952 SCISEARCH
GA The Genuine Article (R) Number: 326AT
TI Identification of genes required for chronic persistence of Brucella abortus in mice
AU Hong P C; Tsois R M (Reprint); Ficht T A
CS TEXAS A&M UNIV, COLL VET MED, DEPT VET PATHOBIOL, COLLEGE STN, TX 77843 (Reprint); TEXAS A&M UNIV, COLL VET MED, DEPT VET PATHOBIOL, COLLEGE STN, TX 77843
CYA USA
SO INFECTION AND IMMUNITY, (JUL 2000) Vol. 68, No. 7, pp. 4102-4107.
Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904.
ISSN: 0019-9567.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 32
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 128 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2000:786543 SCISEARCH
 GA The Genuine Article (R) Number: 363CH
 TI Identification of *Streptococcus agalactiae* ***virulence***
 genes in the neonatal rat sepsis model using signature-tagged
 mutagenesis
 AU Jones A L; Knoll K M; Rubens C E (Reprint)
 CS CHILDRENS HOSP & MED CTR, DEPT PEDIAT, DIV INFECT DIS, 4800 SAND POINT WAY
 NE, CH-32, SEATTLE, WA 98105 (Reprint); CHILDRENS HOSP & MED CTR, DEPT
 PEDIAT, DIV INFECT DIS, SEATTLE, WA 98105; UNIV WASHINGTON, SEATTLE, WA
 98105
 CYA USA
 SO MOLECULAR MICROBIOLOGY, (SEP 2000) Vol. 37, No. 6, pp. 1444-1455.
 Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE,
 OXON, ENGLAND.
 ISSN: 0950-382X.
 DT Article; Journal
 FS LIFE
 LA English
 REC Reference Count: 41
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 129 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
 AN 2000:853027 SCISEARCH
 GA The Genuine Article (R) Number: 371LP
 TI Fishing for mycobacterial ***virulence*** ***genes*** : a promising
 animal model
 AU Trucksis M
 CS UNIV MARYLAND, SCH MED, DEPT MED, CTR VACCINE DEV, BALTIMORE, MD 21201
 CYA USA
 SO ASM NEWS, (NOV 2000) Vol. 66, No. 11, pp. 668-674.
 Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904.
 ISSN: 0044-7897.
 DT Article; Journal
 LA English
 REC Reference Count: 9

L4 ANSWER 130 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
 AN 2000:434481 SCISEARCH
 GA The Genuine Article (R) Number: 320UK
 TI In vivo gene expression and the adaptive response: from pathogenesis to
 vaccines and antimicrobials
 AU Heithoff D M; Sinsheimer R L; Low D A; Mahan M J (Reprint)
 CS UNIV CALIF SANTA BARBARA, DEPT MOL CELLULAR & DEV BIOL, SANTA BARBARA, CA
 93106 (Reprint); UNIV CALIF SANTA BARBARA, DEPT MOL CELLULAR & DEV BIOL,
 SANTA BARBARA, CA 93106
 CYA USA
 SO PHILOSOPHICAL TRANSACTIONS OF THE ROYAL SOCIETY OF LONDON SERIES
 B-BIOLOGICAL SCIENCES, (29 MAY 2000) Vol. 355, No. 1397, pp. 633-642.
 Publisher: ROYAL SOC LONDON, 6 CARLTON HOUSE TERRACE, LONDON SW1Y 5AG,
 ENGLAND.
 ISSN: 0962-8436.
 DT Article; Journal
 FS LIFE; AGRI
 LA English
 REC Reference Count: 62
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 131 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
 AN 2000:808350 SCISEARCH
 GA The Genuine Article (R) Number: 366ME
 TI Signature-tagged mutagenesis in the identification of ***virulence***

genes in pathogens

AU Shea J E (Reprint); Santangelo J D; Feldman R G

CS MICROSCI LTD, 545 ESKDALE RD, WOKINGHAM RG41 5TU, BERKS, ENGLAND (Reprint)

CYA ENGLAND

SO CURRENT OPINION IN MICROBIOLOGY, (OCT 2000) Vol. 3, No. 5, pp. 451-458.

Publisher: CURRENT BIOLOGY LTD, 84 THEOBALDS RD, LONDON WC1X 8RR, ENGLAND.

ISSN: 1369-5274.

DT General Review; Journal

FS LIFE; AGRI

LA English

REC Reference Count: 57

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 132 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 12

AN 2000:540447 BIOSIS

DN PREV200000540447

TI Detection of genes essential in specific niches by signature-tagged
mutagenesis.

AU Lehoux, Dario E. (1); Levesque, Roger C. (1)

CS (1) Microbiologie Moleculaire et Genie des Proteines, Faculte de Medecine,
Universite Laval, Pavillon Charles-Eugene Marchand, Sainte-Foy, PQ, G1K
7P4 Canada

SO Current Opinion in Biotechnology, (October, 2000) Vol. 11, No. 5, pp.
434-439. print.

ISSN: 0958-1669.

DT General Review

LA English

SL English

L4 ANSWER 133 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 2000:685428 SCISEARCH

GA The Genuine Article (R) Number: 350MU

TI Life on the inside: Probing Mycobacterium ***tuberculosis*** gene
expression during infection

AU Triccas J A (Reprint); Gicquel B

CS CENTENARY INST CANC MED & CELL BIOL, LOCKED BAG 6, NEWTOWN, NSW 2042,
AUSTRALIA (Reprint); INST PASTEUR, UNITE GENET MYCOBACTERIENNE, PARIS,
FRANCE

CYA AUSTRALIA; FRANCE

SO IMMUNOLOGY AND CELL BIOLOGY, (AUG 2000) Vol. 78, No. 4, pp. 311-317.

Publisher: BLACKWELL SCIENCE ASIA, 54 UNIVERSITY ST, P O BOX 378, CARLTON
VICTORIA 3053, AUSTRALIA.

ISSN: 0818-9641.

DT Article; Journal

FS LIFE

LA English

REC Reference Count: 60

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 134 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 13

AN 2000:773291 CAPLUS

DN 134:339208

TI ***Tuberculosis*** vaccine design: Influence of the completed genome
sequence

AU Montgomery, Donna L.

CS Virus and Cell Biology, Merck and Co., West Point, PA, 19486, USA

SO Briefings in Bioinformatics (2000), 1(3), 289-296

CODEN: BBIMFX; ISSN: 1467-5463

PB Henry Stewart Publications

DT Journal; General Review

LA English

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 135 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2000:517720 CAPLUS

DN 134:97544

TI Genetics of mycobacterial virulence

AU Collins, Desmond M.; Gicquel, Brigitte

CS AgResearch, Wallaceville Animal Research Centre, Upper Hutt, N. Z.

SO Molecular Genetics of Mycobacteria (2000), 265-278. Editor(s): Hatfull,
Graham F.; Jacobs, William R., Jr. Publisher: American Society for
Microbiology, Washington, D. C.

CODEN: 69AEPU

DT Conference; General Review

LA English

RE.CNT 110 THERE ARE 110 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 136 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 14

AN 2001:8792 BIOSIS

DN PREV200100008792

TI An *esat6* knockout mutant of *Mycobacterium bovis* produced by homologous
recombination will contribute to the development of a live
tuberculosis vaccine.

AU Wards, B. J. (1); de Lisle, G. W.; Collins, D. M.

CS (1) Wallaceville Animal Research Centre, AgResearch, Upper Hutt:
wardsb@agresearch.cri.nz New Zealand

SO Tubercle and Lung Disease, (2000) Vol. 80, No. 4-5, pp. 185-189. print.
ISSN: 0962-8479.

DT Article

LA English

SL English

L4 ANSWER 137 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2000:469783 BIOSIS

DN PREV200000469783

TI ***Virulence*** ***genes*** mycobacteria.

AU Nakata, Noboru (1)

CS (1) Department of Microbiology Leprosy Research Center, National Institute
of Infectious Diseases, 4-2-1 Aobacho, Higashimurayama-shi, Tokyo,
189-0002 Japan

SO Japanese Journal of Leprosy, (July, 2000) Vol. 69, No. 2, pp. 61-69.
print.
ISSN: 1342-3681.

DT Article

LA Japanese

SL English

L4 ANSWER 138 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2000:347120 BIOSIS

DN PREV200000347120

TI Strategies to identify in vivo expressed genes and putative virulence
factors in *Mycobacterium* ***tuberculosis***

AU Jones, M. (1); Walters, S.; Smith, I.

CS (1) Southern University, Baton Rouge, LA USA

SO Abstracts of the General Meeting of the American Society for Microbiology,
(2000) Vol. 100, pp. 52. print.
Meeting Info.: 100th General Meeting of the American Society for
Microbiology Los Angeles, California, USA May 21-25, 2000 American Society

for Microbiology
. ISSN: 1060-2011.

DT Conference
LA English
SL English

L4 ANSWER 139 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:640726 CAPLUS
DN 131:253331
TI Methods of identifying bacterial genes that are incompatible with
bacterial pathogenicity and use of such genes as antibacterials
IN Maurelli, Anthony T.; Fernandez, Reinaldo; Fasano, Alessio; Bloch, Craig
A.

PA USA
SO PCT Int. Appl., 53 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9949888	A2	19991007	WO 1999-US6990	19990331
WO 9949888	A3	19991118		
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6344201	B1	20020205	US 1999-281274	19990330
CA 2326391	AA	19991007	CA 1999-2326391	19990331
AU 9932184	A1	19991018	AU 1999-32184	19990331
AU 763993	B2	20030807		
EP 1071412	A2	20010131	EP 1999-914303	19990331
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002509896	T2	20020402	JP 2000-540850	19990331
US 2002192225	A1	20021219	US 2002-34213	20020103
PRAI US 1998-80202P	P	19980331		
US 1999-281274	A3	19990330		
WO 1999-US6990	W	19990331		

L4 ANSWER 140 OF 194 USPATFULL on STN
AN 1999:170593 USPATFULL
TI DNA molecule encoding for cellular uptake of mycobacterium
tuberculosis and uses thereof
IN Riley, Lee W., New York, NY, United States
PA Cornell Research Foundation, Inc., Ithaca, NY, United States (U.S.
corporation)
PI US 6008201 19991228
AI US 1995-464052 19950605 (8)
RLI Division of Ser. No. US 1995-392210, filed on 22 Feb 1995 which is a
continuation-in-part of Ser. No. US 1993-118442, filed on 2 Sep 1993,
now abandoned

DT Utility
FS Granted
EXNAM Primary Examiner: Campbell, Bruce R.; Assistant Examiner: Nguyen, Dave
Trong

LREP Nixon Peabody LLP
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 1541
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 141 OF 194 USPATFULL on STN
AN 1999:132589 USPATFULL
TI TM4 conditional shuttle phasmids and uses thereof
IN Jacobs, Jr., William R., City Island, NY, United States
Bardarov, Stoyan, Bronx, NY, United States
Hatfull, Graham F., Pittsburgh, PA, United States
PA Albert Einstein College of Medicine of Yeshiva University, Bronx, NY,
United States (U.S. corporation)
University of Pittsburgh, Pittsburgh, PA, United States (U.S.
corporation)
PI US 5972700 19991026
AI US 1997-938059 19970926 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Yucel, Irem
LREP Amster, Rothstein & Ebenstein
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 5 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 873
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 142 OF 194 USPATFULL on STN
AN 1999:128349 USPATFULL
TI Mycobacteriophages and uses thereof
IN Bloom, Barry R., Hastings on Hudson, NY, United States
Davis, Ronald W., Palo Alto, CA, United States
Jacobs, Jr., William R., Bronx, NY, United States
Young, Richard A., Winchester, MA, United States
Husson, Robert N., Takoma Park, MD, United States
PA Albert Einstein College of Medicine of Yeshiva University, Bronx, NY,
United States (U.S. corporation)
The Board of Trustees of the Leland Stanford, Jr. University, Stanford,
CA, United States (U.S. corporation)
Whitehead Institute for Biomedical Research, Cambridge, MA, United
States (U.S. corporation)
PI US 5968733 19991019
AI US 1998-14560 19980128 (9)
RLI Continuation of Ser. No. US 1995-463942, filed on 5 Jun 1995, now
patented, Pat. No. US 5854055 which is a continuation of Ser. No. US
1989-361944, filed on 5 Jun 1989, now patented, Pat. No. US 5504005
which is a continuation-in-part of Ser. No. US 1988-223089, filed on 22
Jul 1988, now abandoned And a continuation-in-part of Ser. No. US
1988-216390, filed on 7 Jul 1988, now abandoned which is a
continuation-in-part of Ser. No. US 1988-163546, filed on 3 Mar 1988,
now abandoned which is a continuation-in-part of Ser. No. US 1987-20451,
filed on 2 Mar 1987, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: LeGuyader, John L.
LREP Amster, Rothstein & Ebenstein
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 26 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 2220
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 143 OF 194 USPATFULL on STN
AN 1999:40159 USPATFULL
TI Method, compositions and kit for detection and identification of

microorganisms

IN Lacroix, Jean-Michel, Etobicoke, Canada
Leushner, James, North York, Canada
Hui, May, Toronto, Canada
Dunn, James M., Scarborough, Canada
Larson, Marina T., Yorktown, NY, United States
PA Visible Genetics, Inc., Toronto, Canada (non-U.S. corporation)
PI US 5888736 19990330
AI US 1997-807138 19970227 (8)
RLI Continuation-in-part of Ser. No. US 1996-684498, filed on 19 Jul 1996,
now patented, Pat. No. US 5830657 Ser. No. Ser. No. US 1996-640672,
filed on 1 May 1996, now patented, Pat. No. US 5789168 And Ser. No. US
1995-577858, filed on 22 Dec 1995, now patented, Pat. No. US 5834189
DT Utility
FS Granted
EXNAM Primary Examiner: Elliott, George C.; Assistant Examiner: Larson, Thomas
G
LREP Oppedahl & Larson LLP
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 2556
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 144 OF 194 USPATFULL on STN
AN 1999:27395 USPATFULL
TI Identification of genes
IN Holden, David William, London, United Kingdom
PA RPMS Technology Limited, London, United Kingdom (non-U.S. corporation)
PI US 5876931 19990302
WO 9617951 19760613
AI US 1997-637759 19970719 (8)
WO 1995-GB2875 19951211
19970719 PCT 371 date
19970719 PCT 102(e) date
PRAI GB 1994-24921 19941209
GB 1995-1881 19950131
GB 1995-9239 19950505
DT Utility
FS Granted
EXNAM Primary Examiner: Degen, Nancy; Assistant Examiner: Schwartzman, Robert
LREP Arnall Golden & Gregory LLP
CLMN Number of Claims: 31
ECL Exemplary Claim: 1
DRWN 119 Drawing Figure(s); 112 Drawing Page(s)
LN.CNT 6165
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 145 OF 194 USPATFULL on STN
AN 1999:12561 USPATFULL
TI Recombinant attenuated ALVAC canarypox virus containing heterologous
HIV or SIV inserts
IN Paoletti, Enzo, Delmar, NY, United States
Tartaglia, James, Schenectady, NY, United States
Cox, William I., Troy, NY, United States
PA Virogenetics Corporation, Troy, NY, United States (U.S. corporation)
PI US 5863542 19990126
AI US 1995-417210 19950405 (8)
RLI Continuation-in-part of Ser. No. US 1994-223842, filed on 6 Apr 1994,
now abandoned Continuation-in-part of Ser. No. US 1993-105483, filed on
13 Aug 1993, now patented, Pat. No. US 5494807 which is a continuation

of Ser. No. US 1992-847951, filed on 6 Mar 1992, now abandoned which is a continuation-in-part of Ser. No. US 1991-713967, filed on 11 Jun 1991, now abandoned which is a continuation-in-part of Ser. No. US 1991-666056, filed on 7 Mar 1991, now abandoned, said Ser. No. US 223842 which is a continuation-in-part of Ser. No. US 1992-897382, filed on 11 Jun 1992, now abandoned which is a continuation-in-part of Ser. No. US 1991-715921, filed on 14 Jun 1991, now abandoned

DT Utility

FS Granted

EXNAM Primary Examiner: Stucker, Jeffrey; Assistant Examiner: Parkin, Jeffrey S.

LREP Frommer Lawrence & Haug LLP, Frommer, William S., Kowalski, Thomas J.

CLMN Number of Claims: 17

ECL Exemplary Claim: 1,12,15

DRWN 175 Drawing Figure(s); 128 Drawing Page(s)

LN.CNT 6908

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 146 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 2000:27143 BIOSIS

DN PREV200000027143

TI Attenuation of virulence in Mycobacterium ***tuberculosis***
expressing a constitutively active iron repressor.

AU Manabe, Yukari C.; Saviola, Beatrice J.; Sun, Li; Murphy, John R.; Bishai, William R. (1)

CS (1) Center for Tuberculosis Research, Johns Hopkins School of Public Health, 615 North Wolfe Street, Room 5031C, Baltimore, MD, 21205 USA

SO Proceedings of the National Academy of Sciences of the United States of America, (Oct. 26, 1999) Vol. 96, No. 22, pp. 12844-12848.

ISSN: 0027-8424.

DT Article

LA English

SL English

L4 ANSWER 147 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 1999:762170 SCISEARCH

GA The Genuine Article (R) Number: 241DY

TI Identification of Mycobacterium ***tuberculosis*** RNAs synthesized in response to phagocytosis by human macrophages by selective capture of transcribed sequences (SCOTS)

AU Graham J E; ClarkCurtiss J E (Reprint)

CS WASHINGTON UNIV, DEPT BIOL, CAMPUS BOX 1137, ST LOUIS, MO 63130 (Reprint);
WASHINGTON UNIV, DEPT BIOL, ST LOUIS, MO 63130

CYA USA

SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (28 SEP 1999) Vol. 96, No. 20, pp. 11554-11559.

Publisher: NATL ACAD SCIENCES, 2101 CONSTITUTION AVE NW, WASHINGTON, DC 20418.

ISSN: 0027-8424.

DT Article; Journal

FS LIFE

LA English

REC Reference Count: 48

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 148 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1999:323010 BIOSIS

DN PREV199900323010

TI Solution structure and peptide binding studies of the C-terminal Src homology 3-like domain of the diphtheria toxin repressor protein.

AU Wang, Guangshun; Wylie, Gregory P.; Twigg, Pamela D.; Caspar, Donald L.

D.; Murphy, John R.; Logan, Timothy M. (1)
CS (1) Institute of Molecular Biophysics, Florida State University,
Tallahassee, FL, 32306-4380 USA
SO Proceedings of the National Academy of Sciences of the United States of
America, (May 25, 1999) Vol. 96, No. 11, pp. 6119-6124.
ISSN: 0027-8424.

DT Article
LA English
SL English

L4 ANSWER 149 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 15

AN 2000:34126 BIOSIS
DN PREV200000034126

TI Genomic analysis reveals variation between Mycobacterium
tuberculosis H37Rv and the attenuated M. ***tuberculosis***
H37Ra strain.

AU Brosch, Roland; Philipp, Wolfgang J.; Stavropoulos, Evangelos; Colston, M.
Joseph; Cole, Stewart T.; Gordon, Stephen V. (1)

CS (1) Veterinary Laboratories Agency, Woodham Lane, New Haw, Addlestone,
Surrey, KT15 3NB UK
SO Infection and Immunity, (Nov., 1999) Vol. 67, No. 11, pp. 5768-5774.
ISSN: 0019-9567.

DT Article
LA English
SL English

L4 ANSWER 150 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 1999:744246 CAPLUS
DN 132:118244

TI The Mycobacterium ***tuberculosis*** mysB gene product is a functional
equivalent of the Escherichia coli sigma factor, KatF

AU Mulder, N. J.; Powles, R. E.; Zappe, H.; Steyn, L. M.

CS Department of Medical Microbiology, University of Cape Town, Groote Schuur
Hospital, Observatory, S. Afr.

SO Gene (1999), 240(2), 361-370
CODEN: GENED6; ISSN: 0378-1119

PB Elsevier Science B.V.

DT Journal
LA English

RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 151 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 16

AN 2000:556 BIOSIS
DN PREV20000000556

TI Identification and characterization of two divergently transcribed iron
regulated genes in Mycobacterium ***tuberculosis***

AU Rodriguez, G. Marcela; Gold, B.; Gomez, M.; Dussurget, O.; Smith, I. (1)

CS (1) TB Center, Public Health Research Institute, New York, NY, 10016 USA
SO Tubercle and Lung Disease, (1999) Vol. 79, No. 5, pp. 287-298.

ISSN: 0962-8479.

DT Article
LA English
SL English

L4 ANSWER 152 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 17

AN 1999:509913 BIOSIS
DN PREV199900509913

TI Identification of a ***virulence*** ***gene*** cluster of
Mycobacterium ***tuberculosis*** by signature-tagged transposon
mutagenesis.

AU Camacho, Luis Reinaldo; Ensergueix, Danielle; Perez, Esther; Gicquel,
Brigitte; Guilhot, Christophe (1)

CS (1) Unite de Genetique Mycobacterienne, Institut Pasteur, 25 rue du Dr
Roux, 75724, Paris Cedex 15 France

SO Molecular Microbiology, (Oct., 1999) Vol. 34, No. 2, pp. 257-267.
ISSN: 0950-382X.

DT Article

LA English

SL English

L4 ANSWER 153 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 1999:266833 CAPLUS

DN 131:126006

TI Search for Genes Potentially Involved in Mycobacterium
tuberculosis Virulence by mRNA Differential Display

AU Rindi, Laura; Lari, Nicoletta; Garzelli, Carlo

CS Dipartimento di Patologia Sperimentale, Biotechnologie Mediche,
Infettivologia ed Epidemiologia, Universita di Pisa, Pisa, I-56127, Italy

SO Biochemical and Biophysical Research Communications (1999), 258(1), 94-101
CODEN: BBRCA9; ISSN: 0006-291X

PB Academic Press

DT Journal

LA English

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 154 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 1999:880143 SCISEARCH

GA The Genuine Article (R) Number: 254XC

TI Complex lipid determine tissue specific replication of Mycobacterium
tuberculosis in mice

AU Cox J S; Chen B; McNeil M; Jacobs W R (Reprint)

CS YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT MICROBIOL & IMMUNOL, HOWARD
HUGHES MED INST, BRONX, NY 10461 (Reprint); YESHIVA UNIV ALBERT EINSTEIN
COLL MED, DEPT MICROBIOL & IMMUNOL, HOWARD HUGHES MED INST, BRONX, NY
10461; COLORADO STATE UNIV, DEPT MICROBIOL, FT COLLINS, CO 80523

CYA USA

SO NATURE, (4 NOV 1999) Vol. 402, No. 6757, pp. 79-83.

Publisher: MACMILLAN MAGAZINES LTD, PORTERS SOUTH, 4 CRINAN ST, LONDON N1
9XW, ENGLAND.

ISSN: 0028-0836.

DT Article; Journal

FS PHYS; LIFE; AGRI

LA English

REC Reference Count: 23

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 155 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 18

AN 1998:493192 CAPLUS

DN 129:120090

TI Virulence factors of Mycobacteria and the genes encoding them and their
detection and use

IN Jacobs, William R., Jr.; Bloom, Barry R.; Collins, Desmond Michael; De
Lisle, Geoffrey W.; Pascopella, Lisa; Kawakami, Riku Pamela

PA Agresearch, New Zealand Pastoral Agriculture Research Institute Ltd., N.
Z.; Albert Einstein College of Medicine of Yeshiva University

SO U.S., 74 pp., Cont.-in-part of U.S. Ser. No. 292,695, abandoned.

CODEN: USXXAM

DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI US 5783386	A	19980721	US 1994-363255	19941223
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PRAI US 1994-201880	B2	19940224		
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US 1994-265579	B2	19940624		
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US 1994-292695	B2	19940818		
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RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 156 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 19

AN 1998:441949 CAPLUS

DN 129:91412

TI Conditional shuttle plasmid for based on mycobacteriophage D29 shuttle
plasmid for introduction of DNA into mycobacteria

IN Jacobs, William R.; Hatfull, Graham F.

PA Albert Einstein College of Medicine of Yeshiva University, USA; University
of Pittsburgh

SO U.S., 28 pp., Cont.-in-part of U. S. Ser. No. 247,901.

CODEN: USXXAM

DT Patent
LA English
FAN.CNT 4

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
------------	------	------	-----------------	------

PI US 5773267	A	19980630	US 1996-614770	19960307
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US 5750384	A	19980512	US 1994-247901	19940523
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US 6300061	B1	20011009	US 1996-705557	19960829
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US 6225066	B1	20010501	US 1999-426436	19991025
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PRAI US 1992-833431	B2	19920207		
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US 1993-57531	B2	19930429		
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US 1994-247901	A2	19940523		
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US 1995-430314	B1	19950428		
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US 1996-705557	A1	19960829		
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RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 157 OF 194 USPATFULL on STN

AN 1998:162325 USPATFULL

TI Recombinant mycobacteria

IN Bloom, Barry R., Hastings on Hudson, NY, United States

Jacobs, Jr., William R., Bronx, NY, United States

Davis, Ronald W., Palo Alto, CA, United States

Young, Richard A., Winchester, MA, United States

Husson, Robert N., Takoma Park, MD, United States

PA Albert Einstein College of Medicine of Yeshiva University, a Division of
Yeshiva University, Bronx, NY, United States (U.S. corporation)

PI US 5854055 19981229

AI US 1995-463942 19950605 (8)

RLI Continuation of Ser. No. US 1989-361944, filed on 5 Jun 1989, now
patented, Pat. No. US 5504005 which is a continuation-in-part of Ser.
No. US 1988-223089, filed on 22 Jul 1988, now abandoned And Ser. No. US
1988-216390, filed on 7 Jul 1988, now abandoned, said Ser. No. US
-361944 Ser. No. Ser. No. US -223089 And Ser. No. US -216390 which
is a continuation-in-part of Ser. No. US 1988-163546, filed on 3 Mar
1988, now abandoned which is a continuation-in-part of Ser. No. US
1987-20451, filed on 2 Mar 1987, now abandoned

DT Utility
FS Granted

EXNAM Primary Examiner: Guzo, David; Assistant Examiner: MGarry, Sean
LREP Amster, Rothstein & Ebenstein
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 2205
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 158 OF 194 USPATFULL on STN
AN 1998:128130 USPATFULL
TI Shigella vector for delivering DNA to a mammalian cell
IN Branstrom, Arthur A., Rockville, MD, United States
Sizemore, Donata R., Gaithersburg, MD, United States
Sadoff, Jerald C., Washington, DC, United States
PA The United States of America as represented by the Secretary of the
Army, Washington, DC, United States (U.S. government)
PI US 5824538 19981020
AI US 1995-523855 19950906 (8)
DT Utility
FS Granted

EXNAM Primary Examiner: Lankford, Jr., Leon B.; Assistant Examiner: Tate,
Christopher R.
LREP Harris, Charles H.; Moran, John Francis
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1304

L4 ANSWER 159 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 1998:663611 SCISEARCH
GA The Genuine Article (R) Number: 113PM
TI sigA is an essential gene in Mycobacterium smegmatis
AU Gomez M; Doukhan L; Nair G; Smith I (Reprint)
CS PUBL HLTH RES INST, DEPT MICROBIOL, 455 1ST AVE, NEW YORK, NY 10016
(Reprint); PUBL HLTH RES INST, DEPT MICROBIOL, NEW YORK, NY 10016
CYA USA
SO MOLECULAR MICROBIOLOGY, (JUL 1998) Vol. 29, No. 2, pp. 617-628.
Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 ONE,
OXON, ENGLAND.
ISSN: 0950-382X.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 48

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 160 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1998:418245 BIOSIS
DN PREV199800418245
TI Differentially expressed genes of Mycobacterium ***tuberculosis***
AU Alligood, M. M. (1); Marston, B.; Shinnick, T. M.
CS (1) Emory Univ., Atlanta, GA USA
SO Abstracts of the General Meeting of the American Society for Microbiology,
(1998) Vol. 98, pp. 510.
Meeting Info.: 98th General Meeting of the American Society for
Microbiology Atlanta, Georgia, USA May 17-21, 1998 American Society for
Microbiology
ISSN: 1060-2011.
DT Conference
LA English

L4 ANSWER 161 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 1998:417060 SCISEARCH
GA The Genuine Article (R) Number: ZP880
TI Genetic advances for studying Mycobacterium ***tuberculosis***
pathogenicity
AU Pelicic V (Reprint); Reytrat J M; Gicquel B
CS UNIV PADUA, DIPARTIMENTO SCI BIOMED, I-35121 PADUA, ITALY (Reprint); INST
PASTEUR, UNITE GENET MYCOBACTERIENNE, F-75724 PARIS 15, FRANCE
CYA ITALY; FRANCE
SO MOLECULAR MICROBIOLOGY, (MAY 1998) Vol. 28, No. 3, pp. 413-420.
Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE,
OXON, ENGLAND.
ISSN: 0950-382X.
DT General Review; Journal
FS LIFE
LA English
REC Reference Count: 45
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 162 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 1998:715018 SCISEARCH
GA The Genuine Article (R) Number: 119PR
TI Interdependence of mycobacterial iron regulation, oxidative-stress
response and isoniazid resistance
AU Dussurget O (Reprint); Smith I
CS PUBL HLTH RES INST, 455 1ST AVE, NEW YORK, NY 10016 (Reprint); UNIV PARIS
07, UFR BIOCHIM, F-75251 PARIS 05, FRANCE
CYA USA; FRANCE
SO TRENDS IN MICROBIOLOGY, (SEP 1998) Vol. 6, No. 9, pp. 354-358.
Publisher: ELSEVIER SCI LTD, THE BOULEVARD, LANGFORD LANE, KIDLINGTON,
OXFORD OX5 1GB, OXON, ENGLAND.
ISSN: 0966-842X.
DT General Review; Journal
LA English
REC Reference Count: 34
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 163 OF 194 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS
RESERVED. on STN
AN 1999407862 EMBASE
TI [Direct detection of bacteria in a sample is of great value in case of
slow and difficult growth].
BIOLOGIE MOLECULAIRE ET BACTERIOLOGIE.
AU Bebear C.; Allery A.; Bebear C.M.; De Barbeyrac B.
CS C. Bebear, Hopital Pellegrin, place Amelie-Raba-Leon, 33076 Bordeaux,
France
SO Immuno-Analyse et Biologie Specialisee, (1998) 13/5 (273-278).
Refs: 18
ISSN: 0923-2532 CODEN: IBSPEW
CY France
DT Journal; General Review
FS 004 Microbiology
LA French
SL English; French

L4 ANSWER 164 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:175437 CAPLUS
DN 131:68661
TI A genome-level search for bacterial genes on which positive selection may
operate: a means for identifying possible virulence factors?
AU Gamielidien, Junaid; Hide, Winston

CS South African National Bioinformatics Institute, University of the Western
Cape, Bellville, 7535, S. Afr.
SO Genome Informatics Series (1998), 9, 269-270
CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 165 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN.
AN 1999:632204 SCISEARCH
GA The Genuine Article (R) Number: BN43Y
TI The impact of genomics on the search for novel ***tuberculosis***
drugs
AU Duncan K (Reprint)
CS GLAXO WELLCOME RES & DEV LTD, MED RES CTR, GUNNELS WOOD RD, STEVENAGE SG1
2NY, HERTS, ENGLAND (Reprint)
CYA ENGLAND
SO NOVARTIS FOUNDATION SYMPOSIUM, (AUG 1998) Vol. 217, pp. 228-238.
Publisher: JOHN WILEY & SONS LTD, BAFFINS LANE, CHICHESTER PO19 1UD, WEST
SUSSEX, ENGLAND.
DT Article; Journal
LA English
REC Reference Count: 30
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 166 OF 194 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS
RESERVED. on STN DUPLICATE 20
AN 1999029784 EMBASE
TI [Attenuation of virulence by distribution of the mycobacterium
tuberculosis erp gene].
UNE MUTATION DANS LE GENE ERP ATTENUE LA VIRULENCE DE MYCOBACTERIUM
TUBERCULOSIS
AU Berthet F.-X.; Gicquel B.
CS F.-X. Berthet, SmithKline Beecham Biologicals, Rue de l'Institut, 89-1330
Rixensart, Belgium. berthet@sbbio.be
SO Medecine et Maladies Infectieuses, (1998) 28/SUPPL. DEC. (6-9).
Refs: 6
ISSN: 0399-077X CODEN: MMAIB5
CY France
DT Journal; Conference Article
FS 004 Microbiology
006 Internal Medicine
LA French
SL English; French

L4 ANSWER 167 OF 194 MEDLINE on STN
AN 1998022643 MEDLINE
DN 98022643 PubMed ID: 9359685
TI A green light for ***virulence*** ***gene*** expression.
AU Groisman E A
SO NATURE MEDICINE, (1997 Nov) 3 (11) 1190-1.
Journal code: 9502015. ISSN: 1078-8956.
CY United States
DT News Announcement
LA English
FS Priority Journals
EM 199712
ED Entered STN: 19980109
Last Updated on STN: 19980109

Entered Medline: 19971209

L4 ANSWER 168 OF 194 USPATFULL on STN
AN 97:78182 USPATFULL
TI Invasive microorganisms
IN Falkow, Stanley, Portola Valley, CA, United States
Isberg, Ralph, Brookline, MA, United States
Miller, Virginia, Van Nuys, CA, United States
St. Geme, III, Joseph W., Redwood City, CA, United States
Lee, Catherine A., Newton, MA, United States
PA The Board of Trustees of the Leland Stanford Jr. University, Palo Alto,
CA, United States (U.S. corporation)
PI US 5662908 19970902
AI US 1994-216086 19940321 (8)
RLI Continuation of Ser. No. US 1992-844470, filed on 2 Mar 1992, now
abandoned which is a continuation-in-part of Ser. No. US 1991-644826,
filed on 23 Jan 1991, now patented, Pat. No. US 5239066 which is a
continuation-in-part of Ser. No. US 1990-559904, filed on 30 Jul 1990,
now abandoned which is a continuation-in-part of Ser. No. US
1989-340375, filed on 19 Apr 1989, now patented, Pat. No. US 5310654
which is a continuation-in-part of Ser. No. US 1985-761222, filed on 31
Jul 1985, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Mosher, Mary E.
LREP Flehr, Hohbach, Test, Albritton & Herbert, Trecartin, Richard F., Silva,
Robin M.
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 2673
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 169 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:284814 BIOSIS
DN PREV199799584017
TI Construction of vectors (IVET) for selection of Mycobacterium
tuberculosis genes specifically induced in host tissue.
AU Steyn, A. J. C.; Brown, A. M.; Bloom, B. R.; Jacobs, W. R., Jr.
CS Howard Hughes Med. Inst., Albert Einstein College Med., Bronx, NY 10461
USA
SO Abstracts of the General Meeting of the American Society for Microbiology,
(1997) Vol. 97, No. 0, pp. 562.
Meeting Info.: 97th General Meeting of the American Society for
Microbiology Miami Beach, Florida, USA May 4-8, 1997
ISSN: 1060-2011.
DT Conference; Abstract; Conference
LA English

L4 ANSWER 170 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:284813 BIOSIS
DN PREV199799584016
TI PPTV105, a promoter trap to identify mycobacterial promoters activated
during invasion of the macrophage.
AU Silva-Tatley, Fernanda M. Da; Peiser, Leanne; Ehlers, Mario R. W.
CS Dep. Med. Biochem., Univ. Cape Town Med. Sch., Observatory 7925 South
Africa
SO Abstracts of the General Meeting of the American Society for Microbiology,
(1997) Vol. 97, No. 0, pp. 561.
Meeting Info.: 97th General Meeting of the American Society for
Microbiology Miami Beach, Florida, USA May 4-8, 1997

ISSN: 1060-2011.

DT Conference; Abstract; Conference

LA English

L4 ANSWER 171 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1997:284805 BIOSIS

DN PREV199799584008

TI The KatG gene of Mycobacterium ***tuberculosis*** is associated with growth persistence, and virulence in mice and guinea pigs.

AU Kelley, C. L.; Collins, F. M.; Li, Z.; Rouse, D. A.; Morris, S. L.

CS Lab. Mycobacteria, CBER, FDA, Bethesda, MD USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (1997) Vol. 97, No. 0, pp. 560.

Meeting Info.: 97th General Meeting of the American Society for Microbiology Miami Beach, Florida, USA May 4-8, 1997

ISSN: 1060-2011.

DT Conference; Abstract; Conference

LA English

L4 ANSWER 172 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 97:701159 SCISEARCH

GA The Genuine Article (R) Number: XW009

TI Disruption of IcsP, the major Shigella protease that cleaves IcsA, accelerates actin-based motility

AU Shere K D; Sallustio S; Manassis A; DAversa T G; Goldberg M B (Reprint)

CS YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT MICROBIOL & IMMUNOL, 1300 MORRIS PK AVE, BRONX, NY 10461 (Reprint); YESHIVA UNIV ALBERT EINSTEIN COLL MED, DEPT MICROBIOL & IMMUNOL, BRONX, NY 10461

CYA USA

SO MOLECULAR MICROBIOLOGY, (AUG 1997) Vol. 25, No. 3, pp. 451-462.

Publisher: BLACKWELL SCIENCE LTD, OSNEY MEAD, OXFORD, OXON, ENGLAND OX2 0EL.

ISSN: 0950-382X.

DT Article; Journal

FS LIFE

LA English

REC Reference Count: 39

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 173 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

DUPLICATE 21

AN 1997:366908 BIOSIS

DN PREV199799658841

TI Growth of recombinant Mycobacterium ***tuberculosis*** H37Ra in mouse macrophages.

AU Falcone, V.; Collins, F. (1)

CS (1) Lab. Mycobacteria, CBER/FDA, 1401 Rockville Pike, Rockville, MD 20852 USA

SO Clinical and Experimental Immunology, (1997) Vol. 109, No. 1, pp. 80-83.

ISSN: 0009-9104.

DT Article

LA English

L4 ANSWER 174 OF 194 USPATFULL on STN

AN 96:27116 USPATFULL

TI Recombinant mycobacterial vaccine

IN Bloom, Barry R., Hastings on Hudson, NY, United States

Davis, Ronald W., Palo Alto, CA, United States

Jacobs, Jr., William R., Bronx, NY, United States

Young, Richard A., Winchester, MA, United States

Husson, Robert N., Takoma Park, MD, United States

PA Albert Einstein College of Medicine of Yeshiva University, Bronx, NY,
United States (U.S. corporation)
The Board of Trustees of the Leland Stanford, Jr. University, Stanford,
CA, United States (U.S. corporation)
Whitehead Institute for Biomedical Research, Cambridge, MA, United
States (U.S. corporation)
PI US 5504005 19960402
AI US 1989-361944 19890605 (7)
RLI Continuation-in-part of Ser. No. US 1988-223089, filed on 22 Jul 1988,
now abandoned And Ser. No. US 1988-216390, filed on 7 Jul 1988, now
abandoned , each which is a continuation-in-part of Ser. No. US
1988-163546, filed on 3 Mar 1988, now abandoned which is a
continuation-in-part of Ser. No. US 1987-20451, filed on 2 Mar 1987, now
abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Stone, Jacqueline; Assistant Examiner: LeGuyader, J.
LREP Hamilton, Brook, Smith & Reynolds
CLMN Number of Claims: 29
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 17 Drawing Page(s)
LN.CNT 2391
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 175 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 22
AN 1997:18699 BIOSIS
DN PREV199799317902
TI In search of ***tuberculosis*** ***virulence*** ***genes***
AU Collins, Desmond M.
CS AgRes., Wallaceville Animal Res. Centre, P.O. Box 40063, Upper Hutt New
Zealand
SO Trends in Microbiology, (1996) Vol. 4, No. 11, pp. 426-430.
ISSN: 0966-842X.
DT Journal; Article
LA English

L4 ANSWER 176 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:232153 CAPLUS
DN 124:309067
TI Molecular characterization of a surface-exposed superoxide dismutase of
Mycobacterium avium
AU Escuyer, Vincent; Haddad, Nadia; Frehel, Claude; Berche, Patrick
CS Faculte de Medecine Necker-Enfants Malades, Paris, 75015, Fr.
SO Microbial Pathogenesis (1996), 20(1), 41-55
CODEN: MIPAEV; ISSN: 0882-4010
PB Academic
DT Journal
LA English

L4 ANSWER 177 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 23
AN 1996:197420 BIOSIS
DN PREV199698753549
TI Molecular population genetic analysis of emerged bacterial pathogens:
Selected insights.
AU Musser, James M.
CS Dep. Pathol., Baylor Coll. Med., One Baylor Plaza, Houston, TX 77030 USA
SO Emerging Infectious Diseases, (1996) Vol. 2, No. 1, pp. 1-17.
ISSN: 1080-6040.
DT General Review

LA English

L4 ANSWER 178 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN

AN 1995:820783 CAPLUS

DN 123:222685

TI Virulence factors of Mycobacteria and the genes encoding them and their detection and use

IN Jacobs, William R., Jr.; Bloom, Barry R.; Collins, Desmond Michael; De, Lisle Geoffrey W.; Pascopella, Lisa; Kawakami, Riku Pamela

PA Agresearch New Zealand Pastoral Agriculture Research, N. Z.; Albert Einstein College of Medicine of Yeshiva University

SO PCT Int. Appl., 115 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9517511	A2	19950629	WO 1994-US14912	19941223
WO 9517511	A3	19950727		
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ				
RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2179772	AA	19950629	CA 1994-2179772	19941223
AU 9514458	A1	19950710	AU 1995-14458	19941223
EP 736098	A1	19961009	EP 1995-906122	19941223
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 09510866	T2	19971104	JP 1995-517634	19941223
PRAINZ 1993-250584	A	19931223		
US 1994-201880	A	19940224		
US 1994-265579	A	19940624		
US 1994-292695	A	19940818		
WO 1994-US14912	W	19941223		

L4 ANSWER 179 OF 194 USPATFULL on STN

AN 95:52114 USPATFULL

TI Vaccines containing avirulent phop-type microorganisms

IN Curtiss, III, Roy, St. Louis, MO, United States

Galan, Jorge, St. Louis, MO, United States

PA Washington University, St. Louis, MO, United States (U.S. corporation)

PI US 5424065 19950613

AI US 1992-981935 19921119 (7)

RLI Continuation of Ser. No. US 1989-331979, filed on 31 Mar 1989

DT Utility

FS Granted

EXNAM Primary Examiner: Sidberry, Hazel F.

LREP Rogers, Howell & Haferkamp

CLMN Number of Claims: 10

ECL Exemplary Claim: 1

DRWN 2 Drawing Figure(s); 2 Drawing Page(s)

LN.CNT 1648

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 180 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

DUPLICATE 24

AN 1995:454950 BIOSIS

DN PREV199598469250

TI Mutation of the principal sigma factor causes loss of virulence in a strain of the Mycobacterium ***tuberculosis*** complex.
AU Collins, Desmond M. (1); Kawakami, R. Pamela; De Lisle, Geoffrey W.; Pascopella, Lisa; Bloom, Barry R.; Jacobs, William R., Jr.
CS (1) AgRes., Wallaceville Animal Res. Centre, PO Box 40063, Upper Hutt New Zealand
SO Proceedings of the National Academy of Sciences of the United States of America, (1995) Vol. 92, No. 17, pp. 8036-8040.
ISSN: 0027-8424.
DT Article
LA English

L4 ANSWER 181 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:904921 CAPLUS
DN 124:47036

TI A species-specific nucleotide sequence of Mycobacterium ***tuberculosis*** encodes a protein that exhibits hemolytic activity when expressed in Escherichia coli
AU Leao, Sylvia Cardoso; Rocha, Claudia Lucia; Murillo, Luis Angel; Parra, Carlos Alberto; Patarroyo, Manuel Elkin
CS Inst. de Immunologia-Hospital San Juan de Dios, Univ. Nacional de Colombia, Bogota, Colombia
SO Infection and Immunity (1995), 63(11), 4301-6
CODEN: INFIBR; ISSN: 0019-9567
PB American Society for Microbiology
DT Journal
LA English

L4 ANSWER 182 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1995:147948 BIOSIS
DN PREV199598162248
TI Construction of a promoter trap to identify ***virulence*** ***genes*** in Mycobacterium ***tuberculosis***.
AU Da Silva-Tatley, Fernanda M.; Ehlers, Mario R. W.
CS Dep. Med. Biochem, Univ. Cape Town, Med. Sch., Observatory 7925 South Africa
SO Journal of Cellular Biochemistry Supplement, (1995) Vol. 0, No. 19B, pp. 74.
Meeting Info.: Keystone Symposium on Molecular Mechanisms in Tuberculosis
Tamarron, Colorado, USA February 19-25, 1995
ISSN: 0733-1959.
DT Conference
LA English

L4 ANSWER 183 OF 194 USPATFULL on STN
AN 94:71123 USPATFULL
TI Yersinia INV nucleic acids
IN Isberg, Ralph R., Brookline, MA, United States
Miller, Virginia, Los Angeles, CA, United States
Falkow, Stanley, Portola Valley, CA, United States
PA The Board of Trustees of Leland Stanford Jr. University, Stanford, CA, United States (U.S. corporation)
PI US 5338842 19940816
AI US 1992-890317 19920522 (7)
RLI Continuation of Ser. No. US 1990-559904, filed on 30 Jul 1990, now abandoned which is a continuation-in-part of Ser. No. US 1989-340375, filed on 19 Apr 1989 which is a continuation-in-part of Ser. No. US 1985-761222, filed on 31 Jul 1985, now abandoned
PRAI WO 1990-US2131 19900418
DT Utility
FS Granted

EXNAM Primary Examiner: Schwartz, Richard A.; Assistant Examiner: Mosher, Mary E.

LREP Flehr, Hohbach, Test, Albritton & Herbert

CLMN Number of Claims: 15

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 1821

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 184 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

AN 1994:513655 BIOSIS

DN PREV199497526655

TI Methods for the identification of ***virulence*** ***genes***
expressed in Mycobacterium ***tuberculosis*** strain H37Rv.

AU Kikuta-Oshima, Lynne C.; King, C. Harold; Shinnick, Thomas M.; Quinn,
Frederick D.

CS Natl. Cent. Infect. Dis., CDC Prevent., Atlanta, GA 30333 USA

SO Ades, E. W. [Editor]; Rest, R. F. [Editor]; Morse, S. A. [Editor]. Annals
of the New York Academy of Sciences, (1994) Vol. 730, pp. 263-265. Annals
of the New York Academy of Sciences; Microbial pathogenesis and immune
response.

Publisher: New York Academy of Sciences 2 East 63rd Street, New York, New
York 10021, USA.

Meeting Info.: Conference Orlando, Florida, USA September 8-11, 1993

ISSN: 0077-8923. ISBN: 0-89766-896-0 (paper), 0-89766-895-2 (cloth).

DT Book; Conference

LA English

L4 ANSWER 185 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 25

AN 1995:186527 CAPLUS

DN 122:307465

TI Methods for the identification of ***virulence*** ***genes***
expressed in Mycobacterium ***tuberculosis*** strain H37Rv

AU Kikuta-Oshima, Lynne C.; King, C. Harold; Shinnick, Thomas M.; Quinn,
Frederick D.

CS National Center Infectious Diseases, Centers Disease Control and
Prevention, Atlanta, GA, 30333, USA

SO Annals of the New York Academy of Sciences (1994), 730(MICROBIAL
PATHOGENESIS AND IMMUNE RESPONSE), 263-5

CODEN: ANYAA9; ISSN: 0077-8923

DT Journal

LA English

L4 ANSWER 186 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

AN 94:301378 SCISEARCH

GA The Genuine Article (R) Number: NL287

TI FACTORS CONTROLLING EXPRESSION OF ***VIRULENCE*** ***GENES*** IN
LISTERIA-MONOCYTOGENES

AU DATTA A R (Reprint)

CS US FDA, CTR FOOD SAFETY & APPL NUTR, DIV MOLEC BIOL RES & EVAL, 200 C ST
SW, WASHINGTON, DC, 20204 (Reprint)

CYA USA

SO FOOD MICROBIOLOGY, (APR 1994) Vol. 11, No. 2, pp. 123-129.

ISSN: 0740-0020.

DT Article; Journal

FS AGRI

LA ENGLISH

REC Reference Count: 35

L4 ANSWER 187 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 26

AN 1994:191622 BIOSIS
DN PREV199497204622
TI Methods for the identification of ***virulence*** ***genes***
expressed in Mycobacterium ***tuberculosis*** strain H37RV.
AU Kikuta-Oshima, Lynne C.; King, C. Harold; Shinnick, Thomas M.; Quinn,
Frederick D.
CS Div. Bacterial and Mycotic Dis., Natl. Cent. Infectious Dis., Cent. Dis.
Control and Prevention, Atlanta, GA 30333 USA
SO Journal of Cellular Biochemistry Supplement, (1994) Vol. 0, No. 18 PART A,
pp. 66.
Meeting Info.: Keystone Symposium on Molecular Events in Microbial
Pathogenesis Santa Fe, New Mexico, USA January 8-14, 1994
ISSN: 0733-1959.
DT Conference
LA English

L4 ANSWER 188 OF 194 USPATFULL on STN
AN 93:69992 USPATFULL
TI Yersinia ail nucleic acids
IN St. Geme, III: Joseph W., Redwood City, CA, United States
Falkow, Stanley, Portola Valley, CA, United States
Isberg, Ralph, Brookline, MA, United States
Miller, Virginia, Van Nuys, CA, United States
PA The Board of Trustees of Leland Stanford Jr. University, Stanford, CA,
United States (U.S. corporation)
PI US 5239066 19930824
AI US 1991-644826 19910123 (7)
RLI Continuation-in-part of Ser. No. US 1990-559904, filed on 30 Jul 1990,
now abandoned which is a continuation-in-part of Ser. No. US
1989-340375, filed on 19 Apr 1989 which is a continuation-in-part of
Ser. No. US 1985-761222, filed on 31 Jul 1985, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Schwartz, Richard A.; Assistant Examiner: Mosher, Mary
E.
LREP Flehr, Hohbach, Test, Albritton & Herbert
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 2096
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 189 OF 194 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:421936 CAPLUS
DN 119:21936
TI Sequence of a newly identified Mycobacterium ***tuberculosis*** gene
encoding a protein with sequence homology to virulence-regulating proteins
AU Gupta, Seema; Tyagi, Anil K.
CS Dep. Biochem., Univ. Delhi, New Delhi, 110021, India
SO Gene (1993), 126(1), 157-8
CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English

L4 ANSWER 190 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 92:644205 SCISEARCH
GA The Genuine Article (R) Number: JV756
TI ISOLATION AND CHARACTERIZATION OF ISONIAZID-RESISTANT MUTANTS OF
MYCOBACTERIUM-SMEGMATIS AND M-AURUM
AU HEYM B; COLE S T (Reprint)
CS INST PASTEUR, GENET MOLEC BACTERIENNE LAB, F-75724 PARIS 15, FRANCE; CHU

PITIE SALPETRIERE, SERV BACTERIOL VIROL, F-75634 PARIS 13, FRANCE
CYA FRANCE
SO RESEARCH IN MICROBIOLOGY, (SEP 1992) Vol. 143, No. 7, pp. 721-730.
ISSN: 0923-2508.

DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 42

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 191 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 27
AN 1992:95697 BIOSIS
DN BA93:52247
TI CHARACTERIZATION OF THE HEAT SHOCK RESPONSE IN MYCOBACTERIUM-BOVIS BCG.
AU PATEL B K R; BANERJEE D K; BUTCHER P D
CS DEP. MED. MICROBIOL., ST. GEORGE'S HOSP. MED. SCH., LONDON SW17 0RE,
UNITED KINGDOM.
SO J BACTERIOL, (1991) 173 (24), 7982-7987.
CODEN: JOBAAY. ISSN: 0021-9193.
FS BA; OLD
LA English

L4 ANSWER 192 OF 194 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 91:371162 SCISEARCH
GA The Genuine Article (R) Number: FU011
TI EXTRACTION AND CHARACTERIZATION OF MESSENGER-RNA FROM MYCOBACTERIA -
IMPLICATION FOR ***VIRULENCE*** ***GENE*** IDENTIFICATION
AU PATEL B K R (Reprint); BANERJEE D K; BUTCHER P D
CS ST GEORGE HOSP, SCH MED, DEPT MED MICROBIOL, LONDON, ENGLAND
CYA ENGLAND
SO JOURNAL OF MICROBIOLOGICAL METHODS, (1991) Vol. 13, No. 2, pp. 99-111.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 40
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L4 ANSWER 193 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 28
AN 1991:90938 BIOSIS
DN BA91:49828
TI TRANSFORMATION OF DISTINCT MYCOBACTERIAL SPECIES BY SHUTTLE VECTORS
DERIVED FROM THE MYCOBACTERIUM-FORTUITUM PAL5000 PLASMID.
AU LAZRAQ R; CLAVEL-SERES S; DAVID H L
CS UNITE TUBERCULOSE MYCOBACTERIES, INST. PASTEUR, 75724 PARIS CEDEX 15, FR.
SO CURR MICROBIOL, (1991) 22 (1), 9-14.
CODEN: CUMIDD. ISSN: 0343-8651.
FS BA; OLD
LA English

L4 ANSWER 194 OF 194 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1976:102243 BIOSIS
DN BA61:2243
TI GENETICS IN MYCOBACTERIA.
AU MIZUGUCHI Y; TOKUNAGA T
SO JPN J BACTERIOL, (1975) 30 (2), 297-314.
CODEN: NSKZAM. ISSN: 0021-4930.
FS BA; OLD
LA Unavailable

=> s tuberculosis and (Rv0822c or Rv3137 or Rv2348c or Rv2181 or Rv1954c or Rv0987 or Rv3268 or Rv2610c or Rv0405 or Rv1664 or Rv1662 or Rv2946c or pks6 or pks8 or pks9 or pks1)

L5 13 TUBERCULOSIS AND (RV0822C OR RV3137 OR RV2348C OR RV2181 OR RV1954C OR RV0987 OR RV3268 OR RV2610C OR RV0405 OR RV1664 OR RV1662 OR RV2946C OR PKS6 OR PKS8 OR PKS9 OR PKS1)

=> dup rem l5

PROCESSING COMPLETED FOR L5

L6 8 DUP REM L5 (5 DUPLICATES REMOVED)

=> d bib ab kwic 1-

YOU HAVE REQUESTED DATA FROM 8 ANSWERS - CONTINUE? Y/(N):y

L6 ANSWER 1 OF 8 USPATFULL on STN

AN 2003:232019 USPATFULL

TI Methods for predicting functional and structural properties of polypeptides using sequence models

IN Sem, Daniel S., San Diego, CA, UNITED STATES

Baker, Brian, Poway, CA, UNITED STATES

Hansen, Mark R., San Diego, CA, UNITED STATES

PI US 2003162219 A1 20030828

AI US 2001-40895 A1 20011228 (10)

PRAI US 2000-367371P 20001229 (60)

DT Utility

FS APPLICATION

LREP CAMPBELL & FLORES LLP, 4370 LA JOLLA VILLAGE DRIVE, 7TH FLOOR, SAN DIEGO, CA, 92122

CLMN Number of Claims: 32

ECL Exemplary Claim: 1

DRWN 27 Drawing Page(s)

LN.CNT 7513

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention provides a method for identifying a polypeptide that binds a ligand. The method includes the steps of (a) comparing a sequence of a polypeptide to a sequence model for polypeptides that bind a ligand, wherein the sequence model comprises representations of amino acids consisting of a subset of amino acids, the subset of amino acids having one or more atom within a selected distance from a bound ligand in the polypeptides that bind the ligand; and (b) determining a relationship between the sequence and the sequence model, wherein a correspondence between the sequence and the sequence model identifies the polypeptide as a polypeptide that binds the ligand.

DETD . . . binding NAD (P) binding Tyrosine-
Reductase Rossman

Rossmann dependent
Enoyl Acyl Carrier M. 1bvr NAD (P) binding

NAD (P) binding Tyrosine-
Protein Reductase ***Tuberculosis*** Rossman

Rossmann dependent
Enoyl Acyl Carrier Brassica 1cwu NAD (P) binding

NAD (P) binding Tyrosine-
Protein Reductase Napus (rape) Rossman

Rossmann dependent
Enoyl. . . NAD (P) binding Tyrosine-
Protein Reductase Rossman

Rossmann dependent
Enoyl Acyl Carrier Myobacterium 1eny NAD (P) binding

NAD (P) binding Tyrosine-
Protein Reductase ***Tuberculosis*** Rossman

Rossmann dependent
Enoyl Acyl Carrier Mybacterium 1enz NAD (P) binding

NAD (P) binding Tyrosine-
 Protein Reductase ***Tuberculosis*** Rossman
 Rossman dependent
 Enoyl Acyl Carrier E. coli 1qg6 NAD (P) binding
 NAD (P) binding Tyrosine-
 Protein Reductase Rossman
 Rossman dependent
 Enoyl Acyl. . .
 DETD . . . (polyketide s -25.2 0.82 1
 Rv0242c, 3-oxoacyl-[ACP] reductase, TB.seq, 290666: 29 -25.9 0.95
 1
 Rv0952, succinyl-CoA synthase, TB.seq, 1063138: 1064 -26.1 1
 1
 Rv1662, polyketide synthase, TB.seq, 1881702: 1886507
 -26.5 1.1 1
 Rv3858c, small subunit of NADH-dependent glutamate sy -26.5 1.1
 1
 Rv3391, fatty acyl-CoA reductase, . . . 1387799: 1388 -32.3 3.6
 1
 Rv1350, 3-oxoacyl-[ACP] reductase, TB.seq, 1517489: 1 -32.3 3.7
 1
 Rv3045, alcohol dehydrogenase, TB.seq, 3406282: 34073 -32.5 3.8
 1
 Rv2946c, polyketide synthase, TB.seq, 3291503: 3296350
 -32.6 3.8 1
 Rv3382c, LytB protein homologue, TB.seq, 3796447: 3797 -32.6 3.8
 1
 Rv2787, , TB.seq, 3095108: . . .

L6 ANSWER 2 OF 8 USPATFULL on STN

AN 2002:343879 USPATFULL

TI Novel Polynucleotides

IN Nakagawa, Satoshi, Tokyo, JAPAN

Mizoguchi, Hiroshi, Tokyo, JAPAN

Ando, Seiko, Tokyo, JAPAN

Hayashi, Mikiro, Tokyo, JAPAN

Ochiai, Keiko, Tokyo, JAPAN

Yokoi, Haruhiko, Tokyo, JAPAN

Tateishi, Naoko, Tokyo, JAPAN

Senoh, Akihiro, Tokyo, JAPAN

Ikedo, Masato, Tokyo, JAPAN

Ozaki, Akio, Hofu-shi, JAPAN

PI US 2002197605 A1 20021226

AI US 2000-738626 A1 20001218 (9)

PRAI JP 1999-377484 19991216

JP 2000-159162 20000407

JP 2000-280988 20000803

DT Utility

FS APPLICATION

LREP NIXON & VANDERHYE P.C., 8th Floor, 1100 North Glebe Road, Arlington, VA,
22201

CLMN Number of Claims: 68

ECL Exemplary Claim: 1

DRWN 4 Drawing Page(s)

LN.CNT 13673

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Novel polynucleotides derived from microorganisms belonging to
 coryneform bacteria and fragments thereof, polypeptides encoded by the
 polynucleotides and fragments thereof, polynucleotide arrays comprising
 the polynucleotides and fragments thereof, recording media in which the
 nucleotide sequences of the polynucleotide and fragments thereof have

been recorded which are readable in a computer, and use of them.

SUMM [0011] In recent years, the full nucleotide sequence of the genomes of several microorganisms, such as *Escherichia coli*, *Mycobacterium ***tuberculosis****, yeast, and the like, have been determined (Science, 277:1453-62 (1997); Nature, 393:537-544 (1998); Nature, 387. 5-105 (1997)). Based on the. . .

SUMM . . . fixed to a solid support, have been developed. The techniques contribute to the analysis of microorganisms, such as yeasts, *Mycobacterium ***tuberculosis****, *Mycobacterium bovis* used in BCG vaccines, and the like (Science, 278:680-686 (1997); Proc. Natl. Acad. Sci. USA, 96:12833-38 (1999); Science, . . .

DETD . . . protein)

6	3506	4766	5299	534	sp:YREG_STRCO
	Streptomyces coelicolor yreG				35.1 58.1 174
	hypothetical protein				
7	3507	5354	7486	2133	pir.S44198
	Mycobacterium ***tuberculosis***				71.9 88.9 704
	DNA topoisomerase (ATP-H37Rv gyrB hydrolyzing)				
8	3508	7830	8795	966	
9	3509	9466	8798	669	
10	3510	9562	10071	510	
11	3511	9914	9474	441	
12	3512	11177	10107	1071	sp:YV11_MYCTU
	Mycobacterium ***tuberculosis***				29.4 50.7 422
	NAGC/XYLR repressor H37Rv				
13	3513	11523	11263	261	
14	3514	11768	11523	246	
15	3515	11831	14398	2568	sp:GYRA_MYCTU
	Mycobacterium ***tuberculosis***				70.4 88.1 854
	DNA gyrase subunit A H37Rv Rv0006 gyrA				
16	3516	14405	14746	342	pir.E70698
	Mycobacterium ***tuberculosis***				29.5 69.6 112
	hypothetical membrane protein H37Rv Rv0007				
17	3517	16243	15209	1035	sp:YEIH_ECOLI
	Escherichia coli K12 yehH				33.7 63.5 329. . .
	protein				
21	3521	19497	18736	762	pir:A49232
	Coxiella burnetii com1				31.6 64.5 155
	hypothetical protein				
22	3522	19705	20073	369	pir:F70664
	Mycobacterium ***tuberculosis***				36.8 70.1 117
	repressor H37Rv Rv1846c				
23	3523	20073	21065	993	gp:MLCB1788_6
	Mycobacterium leprae				24.9 50.8 321
	hypothetical membrane protein MLCB1788.18				
24.	38978	39799	822	sp:VIUB_VIBVU	Vibrio
	vulnificus MO6-24 viuB				26.2 52.7 260
	vulnibactin utilization protein				
45	3545	40458	40189	270	sp:YO11_MYCTU
	Mycobacterium ***tuberculosis***				40.0 72.6 95
	hypothetical membrane protein H37Rv Rv0011c				
46	3546	42513	40576	1938	sp:PKNB_MYCLE
	Mycobacterium leprae pknB				40.6 68.7 648

	serine/threonine. . .	1143	sp:SP5E_BACSU	Bacillus		
	subtilis 168 spoVE	31.2	65.6	375	stage V	
	sporulation protein E					
50	3550	48021	46669	1353	pir:H70699	
	Mycobacterium ***tuberculosis***			44.1	70.8	469
	phosphoprotein phosphatase					
	H37Rv ppp					
51	3551	48485	48024	462	pir:A70700	
	Mycobacterium ***tuberculosis***			38.7	66.5	155
	hypothetical protein					
	H37Rv Rv0019c					
52	3552	49368	48505	864	pir:B70700	
	Mycobacterium ***tuberculosis***			23.6	38.8	526
	hypothetical protein					
	H37Rv Rv0020c					
53	3553	49601	49455	147		
54	3554	50616	49897	720		
55	3555	50972	50754	219		
56	3556. . .	3562	57270	56680	591	
	sp:YC61_SYNY3		Synechocystis sp. PCC6803		36.3	70.4
	179		hypothetical protein			
	slr1261					
63	3563	57478	57651	174	pir:G70988	
	Mycobacterium ***tuberculosis***			53.2	83.9	62
	hypothetical protein					
	H37Rv Rv1766					
64	3564	58087	58941	855		
65	3565	59091	59930	840	gp:LMFL4768_11	
	Leishmania major L4768.11		26.8	50.7	310	
	hypothetical protein					
66	3566	59952	60662	711		
67	3567	60669	62321	1653		
68	3568	63508	62390	1119	pir:F70952	
	Mycobacterium ***tuberculosis***			29.5	59.5	390
	magnesium and cobalt transport					
	H37Rv Rv1239c corA					
	protein					
69	3569	64040	63594	447		
70	3570	64190	65458	1269	gp:AF179611_12. .	
	66197	65508	690	sp:PNUC_SALTY		
	Salmonella typhimurium pnuC		24.1	53.1	241	
	required for NMN transport					
72	3572	66851	67972	1122	sp:PHOL_MYCTU	
	Mycobacterium ***tuberculosis***			29.1	60.0	340
	phosphate starvation-induced					
	H37Rv Rv2368C					
	protein-like protein					
73	3573	68170	68301	132		
74	3574	68634	68251	384		
75	3575	69060	69824. . .	SCM2.03		
82	3582	74490	75491	1002	sp:BIOB_CORGL	
	Corynebacterium glutamicum		99.4	99.7	334	
	biotin synthase					
	bioB					
83	3583	75506	75742	237	pir:H70542	
	Mycobacterium ***tuberculosis***			72.1	79.1	43
	hypothetical protein					
	H37Rv Rv1590					
84	3584	75697	76035	339	sp:YK14_YEAST	
	Saccharomyces cerevisiae		34.1	63.5	85	
	hypothetical protein					

YKL084w

85. . .

DET D . . . repressor

accR

124	3624	120021	120410	390	pir:C70019
			57.9	78.6	126
					Bacillus subtilis yurT
					methylglyoxalase
125	3625	120922	120413	510	sp:YC76_MYCTU
				37.0	64.8 162
					Mycobacterium ***tuberculosis***
					hypothetical protein
					H37Rv Rv1276c
126	3626	122459	120951	1509	prf:2309180A
				43.5	70.4 497
					Pseudomonas fluorescens mtlD
					mannitol dehydrogenase
127					glutamine
					2-oxoglutarate
					gltD
					aminotransferase small subunit
209	3709	201580	201341	240	
210	3710	203244	201760	1485	pir:C70793
				44.6	72.8 496
					Mycobacterium ***tuberculosis***
					hypothetical protein
					H37Rv Rv3698
211	3711	205588	205956	369	
212	3712	206068	206385	318	
213	3713	207011	203541	3471	prf:2224383C
				39.8	70.6 1122
					Mycobacterium avium embB
					arabinosyl transferase
214	3714	208989	207007	1983	pir:D70697
				35.0	66.1 651
					Mycobacterium ***tuberculosis***
					hypothetical membrane protein
					H37Rv Rv3792
215	3715	209968	209210	759	prf:2504279B
				31.4	56.5 223
					Pseudomonas sp. phbB
					acetoacetyl CoA reductase
216	3716	211455	209992	1464	pir:B70697
				66.0	85.1 464
					Mycobacterium ***tuberculosis***
					oxidoreductase
					H37Rv Rv3790
217	3717	211768	211535	234	
218	3718	211777	212283	507	
219	3719	212283	212735	453	
220	3720	212656	213657	1002	gp:LMA243459_1
				24.3	57.4 350
					Leishmania major ppgl
					proteophosphoglycan
221	3721	213712	214107	396	sp:YOGN_MYCTU
				60.5	83.9 124
					Mycobacterium ***tuberculosis***
					hypothetical protein
					H37Rv Rv3789
222	3722	214121	214522	402	
223	3723	214527	215159	633	pir:H70666
				43.2	73.8 206
					Mycobacterium ***tuberculosis***
					hypothetical protein
					H37Rv Rv1864c
224	3724	216100	215162	939	pir:B70696
				63.6	79.1 302
					Mycobacterium ***tuberculosis***
					rhamnosyl transferase
					H37Rv Rv3782 rfbE
225	3725	216264	216605	342	
226	3726	216712	216116	597	gp:AB016260_100
				313. . .	217943 804
					Agrobacterium tumefaciens

sp:RFBD_YEREN Yersinia enterocolitica rfbD 31.3 75.6
262 O-antigen export system permease

protein

229 3729 218979 220151 1173 pir:F70695
Mycobacterium ***tuberculosis*** 36.5 63.0 416
hypothetical protein
H37Rv Rv3778c

230 3730 221107 220154 954 gp:AF010309_1
Homo sapiens pig3 41.1 71.5 302
NADPH quinone oxidoreductase

231 3731 221712 221131 582
232 3732 221911 222207 297 PIR:A70606
Mycobacterium ***tuberculosis*** 35.0 51.0 78
probable electron transfer protein
H37Rv Rv3571

233 3733 223685 222210 1476 sp:ALST_BACSU
Bacillus subtilis alsT 46.7 75.8 475. . . 3741
230514 229711 804 prf:2403296E
Arthrobacter nicotinovorans 34.0 68.0 256
molybdate-binding periplasmic
modA
protein

242 3742 230608 230928 321 pir:D70816
Mycobacterium ***tuberculosis*** 37.5 70.8 96
molybdopterin converting factor
H37Rv moaD2
subunit I

243 3743 231842 230931 912 prf:2518354A
Thermococcus litoralis malK 34.3 60.8. . .
DETD Mycobacterium ***tuberculosis*** 46.1 69.1 317
oxidoreductase
H37Rv tyrA

256 3756 242910 243431 522 pir:B70800
Mycobacterium ***tuberculosis*** 48.8 73.8 160
hypothetical protein
H37Rv Rv3753c

257 3757 243494 243910 417 gp:RHBNFXP_1
Bradyrhizobium japonicum 45.1 70.1 144
nitrogen fixation protein

258 3758 244015 244215 201
259 3759 244466 244816 351
260 3760 244902 247304 2403 sp:YV34_MYCTU
Mycobacterium ***tuberculosis*** 20.7 45.7 997
membrane transport protein
H37Rv Rv0507 mmpL2

261 3761 247310 248572 1263 sp:TGT_ZYMMO
Zymomonas mobilis 41.3 68.0 400
queuine. . . 3778 264566 263298 1269
prf:2503462C Heliobacillus mobilis murC 31.3 60.6
444 UDP-N-acetylmuramyl tripeptide

synthetase

279 3779 265678 264599 1080 pir:H70794
Mycobacterium ***tuberculosis*** 25.7 55.2 346
DNA polymerase III epsilon chain
H37Rv dnaQ

280 3780 269124 268258 867 sp:YLEU_CORGL
Corynebacterium glutamicum 100.0 100.0 270. . . 3804
289796 289131 666 sp:CZCR_ALCEU Alcaligenes
eutrophus CH34 38.6 70.4 223

transcriptional activator
 czcR
 305 3805 291243 289777 1467 prf:2214304B
 Mycobacterium ***tuberculosis*** 26.7 56.8 521
 two-component system sensor
 mtrB
 histidine kinase
 306 3806 291815 292417 603 sp:APL_LACLA
 Lactococcus lactis MG1363 apl 28.3 60.0 . . 3813
 297631 297783 153 gp:SCH17_10
 Streptomyces coelicolor A3(2) 84.0 96.0 50
 hypothetical protein
 SCH17.10c
 314 3814 297792 298250 459 pir:G70790
 Mycobacterium ***tuberculosis*** 65.1 89.9 149
 transcriptional regulator
 H37Rv Rv3678c
 315 3815 299684 298332 1353 sp:SHIA_ECOLI
 Escherichia coli K12 shiA 37.3 68.9 440
 shikimate. . . oxidase
 322 3822 305288 305758 471 sp:NODN_RHILV
 Rhizobium leguminosarum nodN 45.8 72.6 153
 nodulation protein
 323 3823 305858 306700 843 pir:F70790
 Mycobacterium ***tuberculosis*** 41.2 72.4 272
 hydrolase
 H37Rv Rv3677c
 324 3824 306367 305195 1173
 325 3825 306800 307504 705
 326 3826 307462 306782 681 prf:2323349A
 Vibrio. . . 3828 307955 308734 780
 sp:UVEN_MICLU Micrococcus luteus pdg 57.5 77.1
 240 ultraviolet N-glycosylase/AP lyase
 329 3829 308745 309302 558 pir:B70790
 Mycobacterium ***tuberculosis*** 34.6 58.3 211
 cytochrome c biogenesis protein
 H37Rv Rv3673c
 330 3830 309370 310038 669 sp:YEAB_ECOLI
 Escherichia coli K12 yeaB 30.7 56.3 192
 hypothetical protein
 331 3831 310135 311325 1191 pir:H70789
 Mycobacterium ***tuberculosis*** 38.6 71.0 396
 serine proteinase
 H37Rv Rv3671c
 332 3832 312891 311899 993 prf:2411250A
 Corynebacterium sp. C12 cEH 29.6 52.1 280
 epoxide hydrolase
 333 3833 313457 312909 549 pir: F70789
 Mycobacterium ***tuberculosis*** 46.8 77.6 156
 hypothetical membrane protein
 334 3834 314590 313625 966 pir:S72914
 Mycobacterium leprae 29.6 65.5 287
 phosphoserine phosphatase
 MTCY20G9.32C. serB
 335 3835 314980 316002 1023 pir:E70788
 Mycobacterium ***tuberculosis*** 35.0 60.2 349
 hypothetical protein
 H37Rv Rv3660c
 336 3836 316110 317132 1023 pir:C44020
 Escherichia coli trbB 32.9 66.5 319
 conjugal transfer region protein

337	3837	316964	316350	615		
338	3838	317078	317893	816	pir:C70788	
	Mycobacterium	***tuberculosis***		30.5	63.7	262
	hypothetical membrane protein					
	H37Rv Rv3658c					
339	3839	317920	318465	546	pir:B70788	
	Mycobacterium	***tuberculosis***		33.8	64.2	201
	hypothetical protein					
	H37Rv Rv3657c					
340	3840	318492	318689	198	pir:A70788	
	Mycobacterium	***tuberculosis***		47.5	84.8	59
	hypothetical protein					
	H37Rv Rv3656c					
341	3841	318696	319013	318		
342	3842	318958	318545	414		
343	3843	318991	319335	345		
344	3844.	. . . Arthrobacter globiformis S155		68.7	88.1	
67		cold shock protein				
	csp					
346	3846	322216	321992	225		
347	3847	322910	325897	2988	pir:G70563	
	Mycobacterium	***tuberculosis***		61.7	81.6	977
	DNA topoisomerase I					
	H37Rv Rv3646c topA					
348	3848	325904	326614	711		
349	3849	327735	326695	1041	sp:CYAB_STIAU	
	Stigmatella aurantiaca. . . protein					
362	3862	338793	339725	933	prf:2512357B	
	Actinoplanes sp. acbB		33.8	66.3	320	
	dTDP-glucose 4,6-dehydratase					
363	3863	340569	340195	375	pir:A70562	
	Mycobacterium	***tuberculosis***		59.3	88.9	108
	hypothetical protein					
	H37Rv Rv3632					
364	3864	341327	340569	759	sp:YC22_METJA	
	Methanococcus jannaschii JAL-		33.9	66.5	230	
	dolichol phosphate. . . ushA		26.1	54.4	586	
	UDP-sugar hydrolase					
368	3868	345975	345814	162		
369	3869	346460	346110	351		
370	3870	348019	346961	1059	sp:ADH_MYCTU	
	Mycobacterium	***tuberculosis***		52.2	74.9	343
	NADP-dependent alcohol					
	H37Rv adhC					
	dehydrogenase					
371	3871	348952	348098	855	sp:RFBA_SALAN	
	Salmonella anatum M32 rfbA		62.8	84.9	285. . . 945	
	prf:2510361A	Staphylococcus aureus sirA		33.2	66.5	
	325	Fe-regulated protein				
376	3876	354387	353749	639		
377	3877	355906	354599	1308	sp:Y17M_MYCTU	
	Mycobacterium	***tuberculosis***		37.4	68.3	423
	hypothetical membrane protein					
	H37Rv Rv3630					
378	3878	357228	355849	1380	gp:SC5F2A_19	
	Streptomyces coelicolor		34.1	62.5	461	
	metallopeptidase					
	SC5F2A.19c					
379. . .						
DET D	. . . glutamicum		75.7	94.3	70	
	transposase (insertion sequence)					

ATCC 31831
IS31831)

398	3898	378562	378287	276			
399	3899	379837	378668	1170	pir:G70539		
	Mycobacterium	***tuberculosis***		28.0	57.4	404	
	hypothetical protein						
	H37Rv Rv1565c						
400	3900	380842	379850	993	gsp:W37352		
	Pseudomonas aeruginosa PAO1			34.5	60.2	354	
	acetyltransferase						
	psbC						
401.	3910	390233	390730	498	gp:PAU49666_2		
	Pseudomonas aeruginosa PAO1			43.8	71.9	153	
	regulatory protein						
	orfX						
411	3911	392208	390787	1422	pir:E70828		
	Mycobacterium	***tuberculosis***		57.0	81.3	477	
	transcriptional regulator						
	H37Rv Rv0465c						
412	3912	392705	393475	771	gp:SCM10_12		
	Streptomyces coelicolor A3(2)			34.8	67.4	230	
	cytochrome b.	3932	406550	407416		867	
	prf:2413441K	Mycobacterium avium GIR10			26.8	53.6	
	280	hypothetical protein					
	mav346						
433	3933	407708	407409	300	pir:A70907		
	Mycobacterium	***tuberculosis***		58.7	85.9	92	
	hypothetical protein						
	H37Rv Rv0190						
434	3934	408546	409145	600			
435	3935	409975	407711	2265	sp:CTPB_MYCLE		
	Mycobacterium leprae ctpB			45.7	429438	2586	
	gp:SCE25_30	Streptomyces coelicolor A3(2)			31.3	60.7	
	921	ABC transporter ATP-binding protein					
	SCE25.30						
457	3957	433028	432126	903	sp:YV21_MYCTU		
	Mycobacterium	***tuberculosis***		45.0	66.9	269	
	cytochrome P450						
	H37Rv RV3121						
458	3958	433062	433988	927	prf:2512277A		
	Pseudomonas aeruginosa ppx			28.8	57.8	306	
	exopolyphosphatase						
459	3959	434010	434822	813	sp:YV23_MYCTU		
	Mycobacterium	***tuberculosis***		28.8	57.3	302	
	hypothetical membrane protein						
	H37Rv Rv0497						
460	3960	434886	435695	810	sp:PROC_CORGL		
	Corynebacterium glutamicum			100.0	100.0	269	
	pyrroline-5-carboxylate reductase						
	618						
467	3967	438044	436980	1065	pir:S72914		
	Mycobacterium leprae			51.0	77.4	296	
	phosphoserine phosphatase						
	MTCY20G9.32C.serB						
468	3968	438179	438424	246	sp:YV35_MYCTU		
	Mycobacterium	***tuberculosis***		40.5	66.2	74	
	hypothetical protein						
	H37Rv Rv0508						
469	3969	438294	438037	258			
470	3970	438516	439904	1389	sp:HEM1_MYCLE		
	Mycobacterium leprae hema			44.4	3993	463867	

464472	606	sp:PMG2_ECOLI	Escherichia coli K12
gpmB	28.0	62.7	161 phosphoglycerate
mutase			
494	3994	464482	465102 621 pir:A70545
Mycobacterium	***tuberculosis***	44.7	71.2 208
hypothetical protein			
H37Rv Rv0526			
495	3995	465118	465909 792 pir:B70545
Mycobacterium	***tuberculosis***	53.5	85.3 245
cytochrome c-type biogenesis			
H37Rv ccsA			
protein			
496	3996	465949	467571 1623 pir:C70545
Mycobacterium	***tuberculosis***	50.7	76.0 533
hypothetical membrane protein			
H37Rv Rv0528			
497	3997	467648	468658 1011 pir:070545
Mycobacterium	***tuberculosis***	44.1	77.8 338
cytochrome c biogenesis protein			
H37Rv ccsB			
498	3998	469370	470170 801
499	3999	470184	470654 471 pir:G70790
Mycobacterium	***tuberculosis***	38.9	69.4 144
transcriptional regulator			
H37Rv Rv3678c pb5			
500	4000	471013	470657 357 prf:2420312A
Staphylococcus aureus zntR	31.1	72.2	90
Zn/Co transport repressor			
501	4001	471420	471121 300
502	4002	471515	471847 333 pir:F70545
Mycobacterium	***tuberculosis***	39.0	78.1 82
hypothetical membrane protein			
DETD		478092	879 sp:ALSR_BACSU
Bacillus subtilis 168 alsR	36.9	66.2	293
als operon regulatory protein			
510	4010	479303	478989 315 pir:B70547
Mycobacterium	***tuberculosis***	33.0	64.9 94
hypothetical protein			
H37Rv Rv0543c			
511	4011	480154	480597 444
512	4012	480201	479452 750 gp:SSP277295_9
Sphingomonas sp. LB126 fldB			2-pyrone-4,6-dicarboxylic acid
513	4013	480624	480208 417
514	4014	481001	480624 378
515	4015	481391	481131 261
516	4016	482668	481394 1275 pir:D70547
Mycobacterium	***tuberculosis***	60.0	83.2 410
low-affinity inorganic phosphate			
H37Rv pitA			
transporter			
517	4017	483587	483366 222
518	4018	483942	483637 306
519	4019	485062	484106 4021 485385
485077	309	pir:C70304	Aquifex aeolicus VF5
phhB	37.7	68.8	77 pterin-4a-
carbinolamine dehydratase			
522	4022	486001	487014 1014 pir:D70548
Mycobacterium	***tuberculosis***	54.0	76.7 335
muconate cycloisomerase			
H37Rv Rv0553 menC			
523	4023	487028	488656 1629 sp:MEND_BACSU

	Bacillus subtilis menD	29.4	54.0	606	
	2-oxoglutarate decarboxylase and 2-				
	succinyl-6-hydroxy-2,4-				
	cyclohexadiene-1-carboxylate				
	synthase				
524	4024 488660 489100	441	pir:G70548		
	Mycobacterium ***tuberculosis***	37.2	64.9	148	
	hypothetical membrane protein				
	H37Rv Rv0556				
525	4025 489209 490447	1239	pir:H70548		
	Mycobacterium ***tuberculosis***	22.8	54.2	408	
	alpha-D-mannose-alpha(1-				
	H37Rv pimB				
	6)phosphatidyl myo-inositol				
	monomannoside transferase				
526	4026 490580 491938	1359	sp:CYCA_ECOLI		
	Escherichia coli K12 cycA	66.2	. . .	Escherichia coli K12	
	ubiE	37.1	66.7	237	
	ubiquinone/menaquinone				
	biosynthesis methyltransferase				
528	4028 492915 493583	669			
529	4029 493916 492645	1272	pir:D70549		
	Mycobacterium ***tuberculosis***	49.0	76.7	412	
	oxidoreductase				
	H37Rv Rv0561c				
530	4030 494061 495110	1050	sp:HEP2_BACST		
	Bacillus stearothermophilus	39.2	67.1	316	
	heptaprenyl diphosphate synthase				
	ATCC. . . rplA				
535	4035 501436 499925	1512	gp:SC5H4_2		
	Streptomyces coelicolor	23.1	50.2	564	
	regulatory protein				
	SC5H4.02				
536	4036 501577 502920	1344	sp:GABT_MYCTU		
	Mycobacterium ***tuberculosis***	60.5	82.4	443	
	4-aminobutyrate aminotransferase				
	H37Rv RV2589 gabT				
537	4037 502925 504283	1359	sp:GABD_ECOLI		
	Escherichia coli K12 gabD	40.8	71.8	461. . .	
	505569 1191	sp:TYRP_ECOLI		Escherichia coli K12	
	o341#7 25.5 49.9 447			tyrosine-specific	
	transport protein				
	tyrP				
540	4040 505698 507647	1950	sp:CTPG_MYCTU		
	Mycobacterium ***tuberculosis***	33.2	64.4	615	
	cation-transporting ATPase G				
	H37Rv RV1992C ctpG				
541	4041 507669 509081	1413	sp:P49_STRLI		
	Streptomyces lividans P49	40.2	66.2	468. . .	
	510510 513	sp:RL10_STRGR		Streptomyces griseus	
	N2-3-11 52.9 84.7 170			50S ribosomal protein	
	L10				
	rplJ				
544	4044 510591 510974	384	sp:RL7_MYCTU		
	Mycobacterium ***tuberculosis***	72.3	89.2	130	
	50S ribosomal protein L7/L12				

H37Rv RV0652 rplL
545 4045 511126 510989 138
546 4046 511536 512507 972 pir:A70962
Mycobacterium ***tuberculosis*** 25.8 55.5 283
hypothetical membrane protein
H37Rv Rv0227c
547 4047 512913 516407 3495 sp:RPOB_MYCTU
Mycobacterium ***tuberculosis*** 75.4 90.4 1180
DNA-directed RNA polymerase beta
H37Rv RV0667 rpoB
chain
548 4048 516494 520492 3999 sp:RPOC_MYCTU
Mycobacterium ***tuberculosis*** 72.9 88.7 1332
DNA-directed RNA polymerase beta
H37Rv RV0668 rpoC
chain
549 4049 519277 518696 582 GP:AF121004_1
Mycobacterium ***tuberculosis*** 39.0 52.0 169
hypothetical protein
H37Rv Jv0166c
550 4050 520671 520850 180
551 4051 520865 521644 780 gp:SCJ9A_15
Streptomyces coelicolor A3(2) 39.2 63.8 232
DNA-binding protein
SCJ9A.15c
552 4052 522476 521679 798 sp:YT08_MYCTU
Mycobacterium ***tuberculosis*** 29.3 57.7 215
hypothetical protein
H37Rv RV2908C
553 4053 522694 523059 366 sp:RS12_MYCIT
Mycobacterium intracellulare 90.9 97.5 121
30S ribosomal protein. . . 535915 840 sp:RL2_MYCLE
Mycobacterium bovis BCG rplB 80.7 92.9 280
50S ribosomal protein L2
572 4072 535935 536210 276 sp:RS19_MYCTU
Mycobacterium ***tuberculosis*** 87.0 98.9 92
30S ribosomal protein S19
H37Rv Rv0705 rpsS
573 4073 536183 535899 285
574 4074 536217 536576 360 sp:RL22_MYCTU
Mycobacterium ***tuberculosis*** 74.3 91.7 109
50S ribosomal protein L22
H37Rv Rv0706 rplV
575 4075 536579 537322 744 sp:RS3_MYCBO
Mycobacterium bovis BCG rpsC 77.4 . . protein S17
579 4079 538267 537974 294
580 4080 538698 538381 318
581 4081 539413 538718 696
582 4082 539741 540106 366 sp:RL14_MYCTU
Mycobacterium ***tuberculosis*** 83.6 95.1 122
50S ribosomal protein L14
H37Rv Rv0714 rplN
583 4083 540112 540423 312 sp:RL24_MYCTU
Mycobacterium ***tuberculosis*** 76.2 91.4 105
50S ribosomal protein L24
H37Rv Rv0715 rplX
584 4084 540426 540998 573 sp:RL5_MICLU
Micrococcus luteus rplE 73.6 92.3 . . formate
dehydrogenase H or alpha

chain

591	4091	547329	548084	756	
592	4092	548990	548187	804	
593	4093	550651	548990	1662	sp:YC81_MYCTU
		Mycobacterium ***tuberculosis***		26.9	52.6 624
		ABC transporter ATP-binding protein			
		H37Rv Rv1281c oppD			
594	4094	551844	550699	1146	
595	4095	552927	551854	1074	
596	4096	554129			
DETD		402	sp:RS11_STRCO		Streptomyces coelicolor
	A3(2)	81.3	93.3	134	30S ribosomal protein
		S11			
		SC6G4.06. rpsK			
626	4126	574615	575217	603	prf:2211287F
		Mycobacterium ***tuberculosis***		82.6	93.9 132
		30S ribosomal protein S4			
		H37Rv RV3458C rpsD			
627	4127	575338	576351	1014	sp:RPOA_BACSU
		Bacillus subtilis 168 rpoA	51.1		577057 577923
		867 sp:TRUA_ECOLI			Escherichia coli K12 truA
		37.0 61.1 265			pseudouridylate synthase A
631	4131	578033	580429	2397	pir:G70695
		Mycobacterium ***tuberculosis***		24.8	51.2 786
		hypothetical membrane protein			
		H37Rv Rv3779			
632	4132	580891	580436	456	
633	4133	581221	580919	303	
634	4134	581406	582662	1257	pir:A70836
		Mycobacterium ***tuberculosis***		27.4	53.8 485
		hypothetical protein			
		H37Rv Rv0283			
635	4135	582684	584228	1545	sp:DIM_ARATH
		Arabidopsis thaliana CV DIM	22.8	50.9	505
		cell. . . 589015 587645	1371		pir:T10930
		Streptomyces coelicolor A3(2)	24.0	50.6	516
		hypothetical membrane protein			
		SC3C3.21			
640	4140	589296	592862	3567	pir:E70977
		Mycobacterium ***tuberculosis***		65.0	38.4 1260
		hypothetical membrane protein			
		H37Rv Rv3447c			
641	4141	590411	589590	822	
642	4142	590560	589898	663	
643	4143	592862	593761	900	
644	4144	593935	594258	324	pir:C70977
		Mycobacterium ***tuberculosis***		31.1	69.9 103
		hypothetical protein			
		H37Rv Rv3445c			
645	4145	594293	594580	288	prf:2111376A
		Mycobacterium ***tuberculosis***		36.3	81.3 80
		early secretory antigen target ESAT-			
		6 protein			
646	4146	594939	595379	441	sp:RL13_STRCO
		Streptomyces coelicolor A3(2)	58.6	82.1	234
653	4153	600876	600022	855	pir:S73000
		Mycobacterium leprae	44.0	72.2	259
		hypothetical protein			
		B229_F1_20			
654	4154	600971	602053	1083	sp:ALR_MYCTU
		Mycobacterium ***tuberculosis***		41.6	68.5 368

alanine racemase
H37Rv RV3423C alr

655 4155 602080 602574 495 sp:Y097_MYCTU
Mycobacterium ***tuberculosis*** 48.7 78.6 154
hypothetical protein

H37Rv Rv3422c

656 4156 602811 604409 1599 sp:YIDE_ECOLI
Escherichia coli K12 yidE 28.9 66.2 550
hypothetical. . . protein

657 4157 604470 605708 1239 gp:PSJ00161_1
Propionibacterium shermanii pip 51.3 77.6 411
proline iminopeptidase

658 4158 605718 606392 675 sp:Y098_MYCTU
Mycobacterium ***tuberculosis*** 52.2 75.4 207
hypothetical protein

H37Rv Rv3421c

659 4159 606392 606898 507 sp:RIMI_ECOLI
Escherichia coli K12 rimI 30.3 59.9 132
ribosomal-protein-alanine. . . 606905 607936 1032
sp:GCP_PASHA Pasteurella haemolytica 46.1 75.2
319 O-sialoglycoprotein endopeptidase

SEROTYPE A1 gcp

661 4161 607958 609679 1722 sp:Y115_MYCTU
Mycobacterium ***tuberculosis*** 38.4 59.4 571
hypothetical protein

H37Rv Rv3433c

662 4162 609747 610175 429
663 4163 610268 609816 453
664 4164 610348 610644 297 sp:CH10_MYCTU
Mycobacterium ***tuberculosis*** 76.0 94.0 100
heat shock protein groES

H37Rv RV3418C mopB

665 4165 610659 612272 1614 sp:CH61_MYCLE
Mycobacterium leprae 63.3 85.1 537
heat shock protein groEL

B229_C3_248 groEl

666 4166 611200 610946 255 GP:MSGTCWPA_1
Mycobacterium ***tuberculosis*** 50.0 56.0 76
hypothetical protein

667 4167 612266 611109 1158 GP:MSGTCWPA_9
Mycobacterium ***tuberculosis*** 34.0 45.0 138
hypothetical protein

668 4168 612714 612418 297 gp:AF073300_1
Mycobacterium smegmatis 64.9 88.3 94
regulatory protein

whiB3

669 4169 613156 613719 564 sp:Y09F_MYCTU
Mycobacterium ***tuberculosis*** 55.2 81.6 174
RNA polymerase sigma factor

H37Rv Rv3414c sigD

670 4170 613722 614747 1026
671 4171 615180 614803 378 sp:Y09H_MYCLE
Mycobacterium. . . response

regulator

684 4184 625677 626000 324
685 4185 626558 626070 489
686 4186 627539 626577 963
687 4187 627727 628551 825 pir:B70975
Mycobacterium ***tuberculosis*** 30.9 64.2 201
hypothetical protein

H37Rv Rv3395c
 688 4188 628551 630140 1590 pir:A70975
 Mycobacterium ***tuberculosis*** 37.5 64.1 563
 hypothetical protein
 H37Rv Rv3394c
 689 4189 630810 630151 660
 690 4190 630949 631809 861 gp:SC5B8_20
 Streptomyces coelicolor A3(2) 33.8 . . . Streptomyces coelicolor
 A3(2) 26.1 56.0 468 hypothetical membrane
 protein
 SCE9.01
 713 4213 655834 655097 738
 714 4214 656547 657215 669 pir:C70884
 Mycobacterium ***tuberculosis*** 50.3 76.4 203
 transcriptional repressor
 H37Rv Rv2788 sirR
 715 4215 658002 657205 798 gp:SCG8A_5
 Streptomyces coelicolor A3(2) 34.9 61.7 264
 hypothetical. . . 4219 659543 660538 996
 gp:CDU02617_1 Corynebacterium diphtheriae 31.1 62.2
 357 iron-regulated lipoprotein precursor
 irp1
 720 4220 661120 660650 471 pir:E70971
 Mycobacterium ***tuberculosis*** 62.9 86.1 151
 rRNA methylase
 H37Rv Rv3366 spoU
 721 4221 661166 662017 852 pir:C70970
 Mycobacterium ***tuberculosis*** 70.9 87.4 278
 methylenetetrahydrofolate
 H37Rv Rv3356c fold
 dehydrogenase
 722 4222 662120 662374 255 gp:MLCB1779_8
 Mycobacterium leprae 31.3 76.3 80
 hypothetical membrane. . .
 DETD . . . sp:YJIX_ECOLI Escherichia coli K12 yjiX 40.0
 66.0 50 hypothetical protein
 730 4230 671653 671045 609
 731 4231 671700 672653 954 pir:C70539
 Mycobacterium ***tuberculosis*** 71.0 86.4 317
 hypothetical protein
 H37Rv Rv1130
 732 4232 672665 673576 912 prf:1902224A
 Streptomyces hygroscopicus 41.6 76.2 281
 carboxy phosphoenolpyruvate
 mutase
 733. . . 695077 1137 sp:DACD_SALTY Salmonella
 typhimurium LT2 30.9 57.5 301
 penicillin-binding protein 6B
 dacD
 precursor
 756 4256 697995 696769 1227 pir:F70842
 Mycobacterium ***tuberculosis*** 34.1 70.7 417
 hypothetical protein
 H37Rv Rv3311
 757 4257 698922 698065 858 gp:SC6G10_8
 Streptomyces coelicolor A3(2) 29.4 52.6 323
 hypothetical protein
 . . . 384 gp:SC1A2_11 Streptomyces coelicolor A3(2)
 41.6 66.2 77 bacterial regulatory protein, lacI
 SC1A2.11

family

762 4262 702081 703262 1182 pir:H70841
Mycobacterium ***tuberculosis*** 51.4 80.5 385
N-acyl-L-amino acid amidohydrolase
H37Rv Rv3305c amiA
or peptidase

763 4263 702108 700384 1725 sp:MANB_MYCPI
Mycoplasma pirum BER manB. . . 4265 705211 708630
3420 prf:2415454A Corynebacterium glutamicum
100.0 100.0 1140 pyruvate carboxylase
strain21253 pyc

766 4266 708839 709708 870 sp:YD24_MYCTU
Mycobacterium ***tuberculosis*** 26.2 60.1 263
hypothetical protein
H37Rv Rv1324

767 4267 709793 710278 486 gp:SCF11_30
Streptomyces coelicolor A3(2) 30.7 66.9 127
hypothetical protein
. . . Mycobacterium smegmatis 54.6 78.9 383
citrate synthase
ATCC 607 gltA

774 4274 716660 716286 375
775 4275 718009 716687 1323 pir:B70539
Mycobacterium ***tuberculosis*** 40.8 72.6 456
hypothetical protein
H37Rv Rv1129c

776 4276 718105 718350 246
777 4277 718658 720016 1359
778 4278 721449 720547 903 sp:THTR_CORGL.
protein

780 4280 723338 722925 414 gp:MLCB4_16
Mycobacterium leprae 51.1 76.7 133
hypothetical protein
MLCB4.27c

781 4281 723412 725559 2148 pir:G70539
Mycobacterium ***tuberculosis*** 35.1 63.4 718
hypothetical membrane protein
H37Rv Rv1565c

782 4282 726462 725872 591 sp:YCEF_ECOLI
Escherichia coli K12 yceF 31.8 66.2 192. . . birA
28.7 61.8 293 bifunctional protein (biotin
synthesis

repressor and biotin acetyl-CoA

carboxylase ligase)

787 4287 731312 731797 486 pir:G70979
Mycobacterium ***tuberculosis*** 23.0 58.8 165
hypothetical membrane protein
H37Rv Rv3278c

788 4288 731857 733017 1161 sp:PURK_CORAM
Corynebacterium 69.0 83.8 394
5'-phosphoribosyl-5-amino-4-
ammonia ATCC. . . 25.1 49.9 1783 RNA
helicase
DRB0135

811 4311 757063 757434 372
812 4312 757395 753697 3699
813 4313 758262 757630 633 pir:E70978
Mycobacterium ***tuberculosis*** 31.7 59.2 240
hypothetical protein

H37Rv ***Rv3268***
 814 4314 760796 758364 2433 pir:C71929
 Helicobacter pylori J99 jhp0462 30.0 62.5 720
 hypothetical protein
 815 4315 762468 760906 1563 sp:UVRD_ECOLI
 Escherichia. . . sp:HEPA_ECOLI Escherichia coli K12 hepA
 23.1 48.6 873 RNA polymerase associated protein

 (ATP-dependent helicase)
 823 4323 778711 777158 1554 pir:D70978
 Mycobacterium ***tuberculosis*** 45.5 71.4 527
 hypothetical protein
 H37Rv Rv3267
 824 4324 779014 779910 897 gp:AF187550_1
 Mycobacterium smegmatis 56.4 77.9 289
 dTDP-Rha:a-D-GlcNAc-
 mc2155 wbbL. . . guanylyltransferase
 826 4326 781468 781875 408 gp:AF164439_1
 Mycobacterium smegmatis 73.4 81.9 94
 regulatory protein
 whmD
 827 4327 782617 782162 456 pir:B70847
 Mycobacterium ***tuberculosis*** 48.9 74.8 139
 hypothetical protein
 H37Rv Rv3259
 828 4328 782712 783101 390 gp:SCE34_11
 Streptomyces coelicolor A3(2) 51.5 71.3 136
 hypothetical protein
 . . . SCE34.11c
 829 4329 783184 784557 1374 sp:MANB_SALMO
 Salmonella montevideo M40 38.0 66.3 460
 phosphomannomutase
 manB
 830 4330 784635 785639 1005 pir:B70594
 Mycobacterium ***tuberculosis*** 31.2 56.3 327
 hypothetical protein
 H37Rv Rv3256c
 831 4331 785643 786824 1182 sp:MANA_ECOLI
 Escherichia coli K12 manA 36.9 66.2 420
 mannose-6-phosphate. . .
 DETD . . . 4339 790096 790704 609 sp:KTHY_ARCFU
 Archaeoglobus fulgidus VC-16 25.8 56.0 209
 thymidylate kinase
 AF0061
 840 4340 790732 791409 678 prf:2214304A
 Mycobacterium ***tuberculosis*** 73.7 90.6 224
 two-component system response
 H37Rv Rv3246c mtrA
 regulator
 841 4341 791421 790738 684
 842 4342 791512 793008 1497 prf:2214304B
 Mycobacterium ***tuberculosis*** 53.1 78.9 484
 two-component system sensor
 H37Rv Rv3245c mtrB
 histidine kinase
 843 4343 793008 794711 1704 pir:F70592
 Mycobacterium ***tuberculosis*** 29.6 65.6 595
 lipoprotein
 H37Rv Rv3244c lpqB
 844 4344 794714 795301 588 pir:D70592
 Mycobacterium ***tuberculosis*** 38.0 72.8 213

	hypothetical protein					
	H37Rv Rv3242c					
845	4345	795447	795292	156		
846	4346	795448	796110	663	sp:RR3O_SPIOL	
	Spinacia oleracea CV rps22. . . 99.6 845					
	preprotein translocase SecA subunit					
	(Corynebacterium glutamicum)					
	MJ-233 secA					
848	4348	799020	799691	672		
849	4349	799697	800200	504	pir:A70591	
	Mycobacterium ***tuberculosis*** 47.1 78.8 170					
	hypothetical protein					
	H37Rv Rv3231c					
850	4350	801194	800208	987	pir:F70590	
	Mycobacterium ***tuberculosis*** 64.6 82.9 322					
	hypothetical protein					
	H37Rv Rv3228					
851	4351	802602	801190	1413	gp:AF114233_1	
	Corynebacterium glutamicum 99.0 99.0 461					
	5-enolpyruvylshikimate 3-phosphate					
	ASO19 aroA					
	synthase					
852	4352	802649	803128	480	pir:D70590	
	Mycobacterium ***tuberculosis*** 38.3 63.9 180					
	hypothetical protein					
	H37Rv Rv3226c					
853	4353	802687	802565	123	GP:AF114233_1	
	Corynebacterium glutamicum 100.0 100.0 23					
	5-enolpyruvylshikimate 3-phosphate					
	synthase					
854	4354	804240	803131	1110	pir:G70506	
	Mycobacterium ***tuberculosis*** 21.6 42.4 380					
	hypothetical protein					
	H37Rv Rv0336					
855	4355	804408	805025	618	prf.2515333D	
	Mycobacterium ***tuberculosis*** 61.2 87.2 188					
	RNA polymerase sigma factor					
	sigH					
856	4356	805792	805535	258	pir:D70596	
	Mycobacterium ***tuberculosis*** 78.6 96.4 84					
	regulatory protein					
	H37Rv Rv3219 whiB1					
857	4357	806318	806737	420	pir:B70596	
	Mycobacterium ***tuberculosis*** 33.3 65.1 129					
	hypothetical protein					
	H37Rv Rv3217c					
858	4358	807939	806740	1200	pir:E70595	
	Mycobacterium ***tuberculosis*** 29.6 62.2 415					
	hypothetical protein					
	H37Rv Rv3212					
859	4359	809217	807946	1272	sp:DEAD_KLEPN	
	Klebsiella pneumoniae CG43 37.3 64.0 458					
	DEAD box ATP-dependent RNA					
	dead					
	helicase					
860	4360	809286	809510	225		
861	4361	809549	810394	846	pir:H70594	
	Mycobacterium ***tuberculosis*** 46.4 69.8 291					
	hypothetical protein					
	H37Rv Rv3207c					

862	4362	810405	811163	759	pir:F70594	
	Mycobacterium	***tuberculosis***		37.0	65.9	249
	hypothetical protein					
	H37Rv Rv3205c					
863	4363	811170	814217	3048	pir:G70951	
	Mycobacterium	***tuberculosis***		23.9	48.9	1155
	ATP-dependent DNA helicase					
	H37Rv Rv3201c					
864	4364	812165	811386	780		
865	4365	814204	817422	3219	pir:G70951	
	Mycobacterium	***tuberculosis***		41.4	65.7	1126
	ATP-dependent DNA helicase					
	H37Rv Rv3201c					
866	4366	815541	814210	1332		
867	4367	817519	818523	1005	sp:Y13B_METJA	
	Methanococcus jannaschii JAL-			26.2	64.2	302
	potassium channel					
	1 MJ0138.1					
868	4368	818523	819236	714	pir:E70951	
	Mycobacterium	***tuberculosis***		30.4	58.3	230
	hypothetical protein					
	H37Rv Rv3199c					
869	4369	819254	821287	2034	sp:UVRD_ECOLI	
	Escherichia coli K12 uvrD			32.6	58.8	660
	DNA helicase II					
870	4370	822079	822669	591		
871	4371	822105	821290	816	pir:B70951	
	Mycobacterium	***tuberculosis***		26.8	49.3	280
	hypothetical protein					
	H37Rv Rv3196					
872	4372	822789	823391	603		
873	4373	824125	822680	1446	pir:A70951	
	Mycobacterium	***tuberculosis***		42.8	76.4	474
	hypothetical protein					
	H37Rv Rv3195					
874	4374	824190	825239	1050	pir:H70950	
	Mycobacterium	***tuberculosis***		43.4	74.9	350
	hypothetical protein					
	H37Rv Rv3194					
875	4375	825916	825242	675		
876	4376	826517	825996	522		
877	4377	826616	829570	2955	pir:G70950	
	Mycobacterium	***tuberculosis***		47.2	73.5	1023
	hypothetical protein					
	H37Rv Rv3193c					
878	4378	830985	829627	1359	gp:AE001938_5	
	Deinococcus radiodurans			34.3	57.7	463
	regulatory protein					
	DR0840					
879	1104	sp:RF2_STRCO	Streptomyces coelicolor A3(2)			
	68.0	88.6	359	peptide chain release factor 2		
	prfB					
894	4394	844495	845181	687	pir:E70919	
	Mycobacterium	***tuberculosis***		70.4	91.2	226
	cell division ATP-binding protein					
	H37Rv Rv3102c ftsE					
895	4395	845105	844842	264	PIR:G72510	
	Aeropyrum pernix K1 APE2061			43.0	54.0	72
	hypothetical protein					
896	4396	845198	846097	900	pir:D70919	
	Mycobacterium	***tuberculosis***		40.5	74.8	301

cell division protein
 H37Rv Rv3101c ftsX
 897 4397 846137 846628 492 sp:SMPB_ECOLI
 Escherichia coli K12 smpB 43.5 75.9 . . 863396
 1671 sp:RA25_YEAST Saccharomyces cerevisiae
 30.7 62.3 613 DNA repair helicase
 S288C YIL143C RAD25
 914 4414 867317 865119 2199 pir:F70815
 Mycobacterium ***tuberculosis*** 36.1 65.2 764
 hypothetical protein
 H37Rv Rv0862c
 915 4415 867353 867571 219 pir:G70815
 Mycobacterium ***tuberculosis*** 44.0 62.0 57
 hypothetical protein
 H37Rv Rv0863
 916 4416 867788 868630 843
 917 4417 868399 867803 597 prf:2420502A
 Micrococcus luteus rpf 39.4 . . 828 sp:TSNR_STRAZ
 Streptomyces azureus tsnR 27.9 51.7 319
 rRNA(adenosine-2'-O-)-

 methyltransferase
 926 4426 874944 874069 876
 927 4427 875883 874951 933 sp:YZ11_MYCTU
 Mycobacterium ***tuberculosis*** 32.6 55.1 316
 hypothetical protein
 H37Rv Rv0883c
 928 4428 877112 875985 1128 pir:S71439
 Bacillus circulans ATCC 21783 21.9 52.9 374
 phosphoserine. . . 883647 1653 pir:JC2382
 Pseudomonas fluorescens 26.4 58.1 549
 sodium/proline symporter
 932 4432 883726 884541 816
 933 4433 885388 884549 840 pir:A70657
 Mycobacterium ***tuberculosis*** 49.0 77.4 243
 hypothetical protein
 H37Rv Rv2525c
 934 4434 885672 894578 8907 pir:S55505
 Corynebacterium 63.1 83.4 3026
 fatty-acid synthase
 ammoniagenes fas
 935. . . 4445 904615 905382 768 sp:FPG_SYNEN
 Synechococcus elongatus 29.2 51.0 298
 formamidopyrimidine-DNA
 naegeli mutM
 glycosidase
 946 4446 905389 905796 408 pir:F70816
 Mycobacterium ***tuberculosis*** 55.5 86.7 128
 hypothetical protein
 H37Rv Rv0870c
 947 4447 906391 905792 600 sp:APL_LACLA
 Lactococcus lactis MG1363 apl 38.8 71.9 196
 alkaline. . .
 DETD . . . 4450 909378 907759 1620
 pir:NUEC Escherichia coli JM101 pgi 52.4 77.0
 557 glucose-6-phosphate isomerase
 951 4451 910696 909521 1176 pir:G70506
 Mycobacterium ***tuberculosis*** 24.6 52.3 195
 hypothetical protein
 H37Rv Rv0336
 952 4452 910843 911223 381

953	4453	911163	910855	309	sp:YT26_MYCTU
	Mycobacterium	***tuberculosis***		59.0	85.9 78
	hypothetical protein				
	H37Rv Rv0948c				
954	4454	911226	913514	2289	sp:PCRA_BACST
	Bacillus stearothermophilus		46.1	73.1	763
	ATP-dependent helicase				
	NCA. . . prf:2420410P				Bacillus subtilis 168 yvrO
	43.8	71.4	217		ABC transporter
957	4457	916874	916368	507	
958	4458	917680	916970	711	pir:D70716
	Mycobacterium	***tuberculosis***		43.6	73.3 236
	peptidase				
	H37Rv Rv0950c				
959	4459	917928	919352	1425	sp:YT19_MYCTU
	Mycobacterium	***tuberculosis***		31.1	60.8 434
	hypothetical protein				
	H37Rv Rv0955				
960	4460	918054	917827	228	
961	4461	919330	919956	627	gp:AB003159_2
	Corynebacterium		64.6	86.2	189. . . 188
	molybdopterin biosynthesis cnx1				
	protein (molybdenum cofactor				
	biosynthesis enzyme cnx1)				
980	4480	932290	932487	198	
981	4481	932974	932570	405	sp:MSCL_MYCTU
	Mycobacterium	***tuberculosis***		50.4	77.1 131
	large-conductance				
	H37Rv Rv0985c mscL				
	mechanosensitive channel				
982	4482	933710	933060	651	pir:A70601
	Mycobacterium	***tuberculosis***		28.6	60.0 210
	hypothetical protein				
	H37Rv Rv0990				
983	4483	934302	933733	570	pir:JC4389
	Homo sapiens MTHFS		25.1	59.7	191
	5-formyltetrahydrofolate cyclo-ligase				
984. . .	936615	937274	660		sp:RIMJ_ECOLI
	Escherichia coli K12 rimJ		29.0	54.9	193
	ribosomal-protein-alanine N-				
	acetyltransferase				
987	4487	937382	938401	1020	pir:G70601
	Mycobacterium	***tuberculosis***		30.3	54.8 367
	hypothetical membrane protein				
	H37Rv Rv0996				
988	4488	938427	939626	1200	sp:CYNX_ECOLI
	Escherichia coli K12 cynX		26.6	62.4	380. . .
	939686	940090	405		sp:YG02_HAEIN
	Haemophilus				
	influenzae Rd		32.1	60.6	137
	hypothetical				
	membrane protein				
	HI1602				
991	4491	940041	940754	714	sp:Y05C_MYCTU
	Mycobacterium	***tuberculosis***		25.3	59.6 225
	hypothetical membrane protein				
	H37Rv Rv0093c				
992	4492	940759	941925	1167	sp:CDAS_BACSH
	Bacillus sphaericus E-244		26.8	53.6	444
	cyclomaltodextrinase				

	CDase					
993	4493	943940	942381	1560	pir:E70602	
	Mycobacterium ***tuberculosis***			43.0	75.2	488
	hypothetical membrane protein					
	H37Rv					
994	4494	944009	944833	825	sp:Y19J_MYCTU	
	Mycobacterium ***tuberculosis***			54.0	78.3	272
	hypothetical protein					
	H37Rv Rv1003					
995	4495	946840	948669	1830	sp:SYM_METTH	
	Methanobacterium			33.8	66.7	615
	methionyl-tRNA synthetase					
	thermoautotrophicum Delta. . . 94					
	transposase					
1008	4508	960385	960861	477	pir:TQEC13	
	Escherichia coli K12			41.7	67.6	139
	transposase					
1009	4509	961297	961653	357	sp:YJ94_MYCTU	
	Mycobacterium ***tuberculosis***			62.6	84.6	91
	transcriptional regulator					
	H37Rv Rv1994c					
1010	4510	961629	962249	621	prf.2514367A	
	Staphylococcus aureus cadD			31.7	66.8	205
	cadmium resistance protein					
1011	4511	961662	961321	342		
1012	4512	962809	963639	831	pir:C70603	
	Mycobacterium ***tuberculosis***			46.4	70.7	263
	hypothetical protein					
	H37Rv Rv1008					
1013	4513	963864	964934	1071	pir:D70603	
	Mycobacterium ***tuberculosis***			34.8	63.5	362
	hypothetical protein					
	H37Rv Rv1009 rpf					
1014	4514	964974	965852	879	sp:KSGA_ECOLI	
	Escherichia coli K12 ksgA			34.3	65.3	265
	dimethyladenosine transferase					
1015	4515	965852	966784	933	pir:F70603	
	Mycobacterium ***tuberculosis***			42.5	67.0	315
	isopentenyl monophosphate kinase					
	H37Rv Rv1011					
1016	4516	966591	965950	642		
1017	4517	966828	968660	1833	pir:S47441	
	Saccharopolyspora erythraea			65.5	4518	968667
	969458	792	sp:PDXK_ECOLI	Escherichia coli K12		
	pdxK	40.1	67.4	242	pyridoxine kinase	
1019	4519	969940	969461	480	sp:YX05_MYCTU	
	Mycobacterium ***tuberculosis***			27.0	58.5	159
	hypothetical protein					
	H37Rv Rv2874					
1020	4520	970029	970349	321	gp:SCF1_2	
	Streptomyces coelicolor A3(2)			45.4	78.7	108
	hypothetical protein					
...	4523	973035	972244	792	sp:YXEH_BACSU	
	Bacillus subtilis 168 yxeH			27.2	59.1	276
	hypothetical protein					
1024	4524	973139	974155	1017	pir:E70893	
	Mycobacterium ***tuberculosis***			35.6	70.9	337
	enoyl-CoA hydratase					
	H37Rv echA9					
1025	4525	973957	973304	654		
1026	4526	974186	974962	777		
1027	4527	976176	974965	1212		

1028 4528. . . 4533 982674 982294 381
 gp:NMA6Z2491_214 Neisseria meningitidis NMA 1953 29.8 63.6
 121 hypothetical protein
 1034 4534 983100 984650 1551 pir:A70539
 Mycobacterium ***tuberculosis*** 24.9 48.3 482
 hypothetical protein
 H37Rv Rv1128c
 1035 4535 984910 985845 936
 1036 4536 986510 984864 1647 pir:I59305
 Escherichia coli K12 prfC. . . 4546 995375 994845
 531 sp:PTH_ECOLI Escherichia coli K12 pth
 38.5 63.2 174 peptidyl-tRNA hydrolase
 1047 4547 996126 995527 600 pir:B70622
 Mycobacterium ***tuberculosis*** 47.0 65.0 194
 50S ribosomal protein L25
 H37Rv rplY
 1048 4548 996402 996830 429 sp:LGUL_SALTY
 Salmonella typhimurium D21 28.7 54.6 143. . .
 DETD
 Escherichia coli mdlB 31.3 62.7 632
 multidrug resistance-like ATP-

binding protein, ABC-type transport

protein
 1078 4578 1026396 1024666 1731 sp:YC73_MYCTU
 Mycobacterium ***tuberculosis*** 50.2 81.9 574
 ABC transporter
 H37Rv Rv1273c
 1079 4579 1028886 1026505 2382 sp:YLI3_CORGL
 Corynebacterium glutamicum 100.0 100.0 368
 hypothetical membrane protein
 . . . yabN 33.4 57.4 183 hypothetical
 protein
 1082 4582 1033185 1032760 426
 1083 4583 1033646 1033269 378
 1084 4584 1033954 1034739 786 pir:A70623
 Mycobacterium ***tuberculosis*** 46.5 68.9 241
 lpqU protein
 H37Rv Rv1022 lpqU
 1085 4585 1034949 1036223 1275 sp:ENO_BACSU
 Bacillus subtilis eno 64.5 86.0 422
 enolase. . . 4586 1036159 1036016 144
 PIR:B72477 Aeropyrum pernix K1 APE2459 68.0 58.0
 41 hypothetical protein
 1087 4587 1036316 1036855 540 pir:C70623
 Mycobacterium ***tuberculosis*** 31.9 55.0 191
 hypothetical protein
 H37Rv Rv1024
 1088 4588 1036900 1037445 546 pir:D70623
 Mycobacterium ***tuberculosis*** 59.5 77.8 153
 hypothetical protein
 H37Rv Rv1025
 1089 4589 1037448 1038410 963 sp:GPPA_ECOLI
 Escherichia coli gppA 25.2 55.0 329
 guanosine pentaphosphatase. . . 1041917 993
 sp:RHAR_ECOLI Escherichia coli rhaR 24.8 55.8
 242 transcription activator of L-rhamnose

operon

1096 4596 1042027 1042842 816 pir:F70893

	Mycobacterium ***tuberculosis***	57.8	80.1	282	
	hypothetical protein				
	H37Rv Rv1072				
1097	4597 1043236 1042850	387			
1098	4598 1043747 1043298	450	gp:SCF55_39		
	Streptomyces coelicolor A3(2)	30.0	4599	1044295	
	1043774 522 sp:GREA_ECOLI			Escherichia coli greA	
	35.0 60.1 143			transcription elongation factor	
1100	4600 1044959 1044477	483	pir:G70894		
	Mycobacterium ***tuberculosis***	34.3	72.1	140	
	hypothetical protein				
	H37Rv Rv1081c				
1101	4601 1045158 1046030	873	pir:S44952		
	Streptomyces lincolnensis lmbE	31.7	56.3	300	
	lincomycin-production				
1102	4602 4636 1072441 1071479	963			
	sp:GLPX_ECOLI			Escherichia coli K12 glpX	44.3 75.7
	325 glycerol metabolism				
1137	4637 1072676 1073245	570	pir:B70897		
	Mycobacterium ***tuberculosis***	27.5	56.4	211	
	hypothetical protein				
	H37Rv Rv1100				
1138	4638 1075241 1073340	1902	pir:H70062		
	Bacillus subtilis ywmD	31.3	66.1	227	
	hypothetical protein				
1139	DET D	1103192	498		
1174	4674 1103180 1103524	345			
1175	4675 1103951 1104103	153			
1176	4676 1104923 1105561	639			
1177	4677 1106058 1104103	1956	sp:YT15_MYCTU		
	Mycobacterium ***tuberculosis***	57.9	80.3	655	
	hypothetical protein				
	H37Rv Rv0959				
1178	4678 1107381 1106086	1296	sp:BCHI_RHOSH		
	Rhodobacter sphaeroides ATCC	27.7	52.6	329	
	magnesium chelatase	1107560	1108201	642	
	gp:AMU73808_1			Amycolatopsis methanolica pgm	33.8 62.5
	160 2,3-PDG dependent				
	phosphoglycerate mutase				
1180	4680 1108201 1108905	705	pir:A70577		
	Mycobacterium ***tuberculosis***	38.2	60.7	262	
	hypothetical protein				
	H37Rv Rv2133c				
1181	4681 1108993 1109754	762	gp:STMBCPA_1		
	Streptomyces hygroscopicus	29.4	59.3	248	
	carboxyphosphoenolpyruvate				
	SF1293 BcpA	1109792	1111432	1641	
	sp:TLRC_STRFR			Streptomyces fradiae tlrC	31.7 54.1
	593 tyrosin resistance ATP-binding				
	protein				
1183	4683 1111820 1111425	396	sp:Y06C_MYCTU		
	Mycobacterium ***tuberculosis***	29.4	66.9	136	
	hypothetical protein				
	H37Rv Rv2923c				
1184	4684 1111889 1112230	342	sp:PHNA_ECOLI		
	Escherichia coli K12 MG1655	55.0	82.0	111	
	alkylphosphonate	1116905	1115832	1074	
	gp:RFAJ3152_2			Ruminococcus flavefaciens	43.9 73.4

376	cysteine desulphurase						
	cysteine desulphurase gene						
1189	4689	1117744	1116908	837	sp:NADC_MYCTU		
	Mycobacterium	***tuberculosis***		42.1	68.9	283	
	nicotinate-nucleotide						
	pyrophosphorylase						
1190	4690	1118932	1117751	1182	pir:E69663		
	Bacillus subtilis	nadA	49.3	77.6	361		
	quinolinate synthetase A						
1191	4691	1134472	1132133	2340	sp:UVRA_THETH		
	Thermus thermophilus	unrA	35.5	58.7	946		
	excinuclease ABC subunit A						
1207	4707	1134561	1135055	495	sp:TPX_MYCTU		
	Mycobacterium	***tuberculosis***		57.3	81.7	164	
	thioredoxin peroxidase						
	H37Rv tpx						
1208	4708	1135476	1135691	216			
1209	4709	1136833	1135058	1776			
1210	4710	1137891	1136938	954	sp:YEDI_ECOLI		
	4718	1141273	1142472	1200	sp:YYAD_BACSU		
	Bacillus subtilis	yvaD	23.5	62.4	340		
	hypothetical membrane protein						
1219	4719	1143015	1142479	537	pir:F70559		
	Mycobacterium	***tuberculosis***		43.5	71.4	147	
	hypothetical protein						
	H37Rv Rv1632c						
1220	4720	1143739	1143026	714	pir:F70555		
	Mycobacterium	***tuberculosis***		35.8	62.9	221	
	hypothetical protein						
	H37Rv Rv1157c						
1221	4721	1144118	1146028	1911	sp:TYPA_ECOLI		
	Escherichia coli K12	typA	46.3	76.7	614		
	GTP-binding protein (tyrosine						
	phosphorylated protein A)						
1222	4722	1146097	1147602	1506	pir:F70874		
	Mycobacterium	***tuberculosis***		27.9	54.9	506	
	hypothetical protein						
	H37Rv Rv1166						
1223	4723	1147592	1148461	870	pir:B70875		
	Mycobacterium	***tuberculosis***		38.7	61.9	315	
	hypothetical protein						
	H37Rv Rv1170						
1224	4724	1148445	1148882	438			
1225	4725	1148953	1149267	315	sp:FER_STRGR		
	Streptomyces griseus	fer	78.6		dhpS		
1233	4733	1158524	1159252	729	gp:MLU15180_14		
	Mycobacterium leprae	u1756l	45.7	73.1	245		
	hypothetical protein						
1234	4734	1159267	1159572	306	pir:G70609		
	Mycobacterium	***tuberculosis***		31.3	67.7	99	
	hypothetical protein						
	H37Rv Rv1209						
1235	4735	1159635	1159799	165	gsp:W32443		
	Mycobacterium	***tuberculosis***		72.3	91.5	47	
	antigen TbAAMK, useful in vaccines						

for prevention or treatment of

tuberculosis

1236	4736	1159865	1160728	864	sp:MYRA_MICGR
		Micromonospora griseorubida	39.2	67.8	286
		mycinamicin-resistance gene			
		myrA			
1237	4737	1162231	1160738	1494	sp:SCRB_PEDPE
		Pediococcus pentosaceus. . . rpoE	27.3	57.2	
	194	(sigma-24); heat shock and			
		oxidative stress			
1242	4742	1166576	1167067	492	
1243	4743	1167110	1167577	468	pir:C70508
		Mycobacterium ***tuberculosis***	45.5	73.2	112
		hypothetical protein			
		H37Rv Rv1224			
1244	4744	1168711	1167587	1125	sp:MRP_ECOLI
		Escherichia coli mrp	43.6	72.0	257
		ATPase			
1245	4745	1169325	1168747	579	pir:B70509
		Mycobacterium ***tuberculosis***	60.4	83.8	154
		hypothetical protein			
		H37Rv Rv1231c			
1246	4746	1170610	1169321	1290	pir:C70509
		Mycobacterium ***tuberculosis***	49.8	77.0	434
		hypothetical protein			
		H37Rv Rv1232c			
1247	4747	1170672	1171187	516	pir:A70952
		Mycobacterium ***tuberculosis***	57.9	87.1	140
		hypothetical protein			
		H37Rv Rv1234			
1248	4748	1171206	1171871	666	
1249	4749	1172462	1171869	594	
1250	4750	1176271	1172501	3771	prf:2306367A. . .
	28.8	60.4	1288		ABC transporter or multidrug
		hamster) MDR2			
		resistance protein 2 (P-glycoprotein			
		2)			
1252	4752	1180837	1180121	717	pir:H70953
		Mycobacterium ***tuberculosis***	31.7	72.1	240
		hypothetical protein			
		H37Rv Rv1249c			
1253	4753	1181675	1180872	804	sp:AROE_ECOLI
		Escherichia coli aroE	25.5	61.2	255
		shikimate dehydrogenase			
1254. . .					
DETD		. . . 885			sp:CATA_ACICA
		Acinetobacter calcoaceticus	30.6	59.4	278
		catechol 1,2-dioxygenase			
		catA			
1283	4783	1217374	1216904	471	
1284	4784	1217982	1217443	540	pir:A70672
		Mycobacterium ***tuberculosis***	31.9	58.4	185
		hypothetical protein			
		H37Rv Rv2972c			
1285	4785	1219895	1222996	3102	sp:SNF2_YEAST
		Saccharomyces cerevisiae	24.9	55.4	878
		transcriptional regulator			
		SNF2			
1286. . .	4787	1222986	1223843	858	gp:SCO007731_6
		Streptomyces coelicolor A3(2)	29.6	56.2	203
		hypothetical protein			

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1288	4788	1223887	1225059	1173	pir:E70755
	Mycobacterium	***tuberculosis***		39.2	67.3 395
	phosphoesterase				
	H37Rv Rv1277				
1289	4789	1225066	1227693	2628	sp:Y084_MYCTU
	Mycobacterium	***tuberculosis***		29.7	59.6 915
	hypothetical protein				
	H37Rv Rv1278				
1290	4790	1227587	1227282	306	
1291	4791	1227657	1227340	318	
1292	4792	1227863	1228636	774	gp:AB029896_1.
	IFO- 21.1	45.9	738		extracellular serine
	protease				
	3046 prtS				
	precursor				
1318	4818	1257067	1257750	684	
1319	4819	1257858	1256851	1008	sp:Y0D3_MYCTU
	Mycobacterium	***tuberculosis***		30.8	62.6 334
	hypothetical membrane protein				
	H37Rv Rv1841c				
1320	4820	1259265	1257865	1401	sp:Y0D2_MYCTU
	Mycobacterium	***tuberculosis***		31.6	60.2 472
	hypothetical membrane protein				
	H37Rv Rv1842c				
1321	4821	1259989	1259429	561	gp:PPU242952_2
	Pseudomonas putida	mobA	27.5	52.3	178
	molybdopterin guanine dinucleotide				
synthase					
1322	4822	1261201	1259993	1209	sp:MOEA_ECOLI
	Mycobacterium	***tuberculosis***		32.8	58.2 366
	molybdopterin biosynthesis protein				
	H37Rv Rv0438c moeA				
1323	4823	1262818	1261688	1131	sp:CNX2_ARATH
	Arabidopsis thaliana	cnx2	51.4	73.7	354. . . 837
	sp:HEMK_ECOLI	Escherichia coli K12		31.1	57.9
	280	protoporphyrinogen oxidase			
1331	4831	1269040	1268267	774	
1332	4832	1269396	1270043	648	sp:YD01_MYCTU
	Mycobacterium	***tuberculosis***		62.3	86.0 215
	hypothetical protein				
	H37Rv Rv1301				
1333	4833	1270047	1271192	1146	sp:RFE_ECOLI
	Escherichia coli K12	rfe	31.1	58.4	322
	undecaprenyl-phosphate. . .	1279522	372		sp:ATPE_STRLI
	Streptomyces lividans	atpE.	41.0	73.0	122
	H ⁺ -transporting ATP synthase				
epsilon chain					
1344	4844	1279770	1280240	471	sp:Y02W_MYCTU
	Mycobacterium	***tuberculosis***		38.6	67.4 132
	hypothetical protein				
	H37Rv Rv1312				
1345	4845	1280270	1280959	690	sp:Y036_MYCTU
	Mycobacterium	***tuberculosis***		70.0	85.7 230
	hypothetical protein				
	H37Rv Rv1321				
1346	4846	1280967	1281251	285	GP:SC26G5_35
	Streptomyces coelicolor A3(2)		45.0	56.0	95
	putative ATP/GTP-binding. . . protein				

1347	4847	1281714	1281262	453	sp:YQJC_BACSU
	Bacillus subtilis yqjC		35.8	68.7	134
	hypothetical protein				
1348	4848	1281794	1282105	312	sp:YC20_MYCTU
	Mycobacterium ***tuberculosis***		54.5	79.2	101
	hypothetical protein				
	H37Rv Rv1898				
1349	4849	1282194	1283114	921	sp:YD24_MYCTU
	Mycobacterium ***tuberculosis***		37.9	71.4	301
	thioredoxin				
	H37Rv Rv1324				
1350	4850	1283324	1284466	1143	gp:ECO237695_3
	Escherichia coli K12 ssuD		50.3	74.3	366
	FMNH2-dependent aliphatic				
...	1286999	957	sp:SSUA_ECOLI	Escherichia coli K12	
	ssuA	35.1	62.1	311	sulfonate binding
	protein precursor				
1354	4854	1289473	1287281	2193	sp:GLGB_ECOLI
	Mycobacterium ***tuberculosis***		46.1	72.7	710
	1,4-alpha-glucan branching enzyme				
	H37Rv Rv1326c glgB				
	(glycogen branching enzyme)				
1355	4855	1291007	1289514	1494	sp:AMY3_DICTH
	Dictyoglomus thermophilum		22.9	31.8	87.6
	ferric enterobactin transport ATP-				211

binding protein or ABC transport

	ATP-binding protein				
1358	4858	1293222	1294025	804	pir:C70860
	Mycobacterium ***tuberculosis***		39.6	68.5	260
	hypothetical protein				
	H37Rv Rv3040c				
1359	4859	1294151	1295206	1056	pir:H70859
	Mycobacterium ***tuberculosis***		43.1	70.0	367
	hypothetical protein				
	H37Rv Rv3037c				
1360	4860	1295047	1294436	612	
1361	4861	1295435	1296220	786	sp:FIXA_RHIME
	Rhizobium meliloti fixA		31.2		acetyltransferase
	yhbS				
1369	4869	1301929	1300988	942	
1370	4870	1303123	1301975	1149	
1371	4871	1303299	1303694	396	
1372	4872	1303829	1304923	1095	pir:C70858
	Mycobacterium ***tuberculosis***		61.8	80.9	361
	tRNA (5-methylaminomethyl-2-				
	H37Rv Rv3024c				
	thiouridylate)-methyltransferase				
1373	4873	1304536	1303883	654	
1374	4874	1304932	1305921	990	pir:B70857
	Mycobacterium ***tuberculosis***		33.7	66.0	332
	hypothetical protein				
	H37Rv Rv3015c				
1375	4875	1307384	1305924	1461	sp:TCMA_STRGA
	Streptomyces glaucescens tcmA		30.2	65.8	500
	tetracenomycin C				
DETD	(polydeoxyribonucleotide synthase				

[NAD+]

1378	4878	1311097	1310435	663	pir:H70856
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	Mycobacterium ***tuberculosis***	40.0	70.9	220	
	hypothetical protein				
	H37Rv Rv3013				
1379	4879 1311320 1311616	297	sp:GATC_STRCO		
	Streptomyces coelicolor A3(2)	53.0	64.0	97	
	glutamyl-tRNA(Gln)				
	gatC				
	amidotransferase subunit C				
1380	4880 1311625 1313115	1491	sp:GATA_MYCTU		
	Mycobacterium ***tuberculosis***	74.0	83.0	484	
	glutamyl-tRNA(Gln)				
	H37Rv gatA				
	amidotransferase subunit A				
1381	4881 1313270 1314118	849	sp:VIUB_VIBVU		
	Vibrio vulnificus viuB	28.1	54.0	263. . . 4895	
	1330967 1329891 1077	sp:YQJG_ECOLI		Escherichia	
	coli K12 yqjG	39.8	66.9	317	hypothetical
	protein				
1396	4896 1331102 1331875	774	pir:A70672		
	Mycobacterium ***tuberculosis***	39.3	62.4	234	
	hypothetical protein				
	H37Rv Rv2972c				
1397	4897 1331953 1333008	1056	pir:H70855		
	Mycobacterium ***tuberculosis***	27.4	52.6	325	
	hypothetical membrane protein				
	H37Rv Rv3005c				
1398	4898 1333424 1333188	237			
1399	4899 1335280 1333442	1839	gp:AJ012293_1		
	Corynebacterium glutamicum	99.2	99.4	613	
	dihydroxy-acid dehydratase				
	ATCC 13032 ilvD				
1400	4900 1335975 1335412	564	pir:G70855		
	Mycobacterium ***tuberculosis***	33.3	68.6	105	
	hypothetical protein				
	H37Rv Rv3004				
1401	4901 1337567 1336095	1473	sp:YILV_CORGL		
	Corynebacterium glutamicum	100.0	100.0	62	
	hypothetical membrane protein				
. . .	sp:LEUD_SALTY	Salmonella typhimurium		67.7	
	89.2 195	3-isopropylmalate dehydratase small			
	subunit				
1454	4954 1382819 1382502	318			
1455	4955 1383798 1382845	954	gp:MLCB637_35		
	Mycobacterium ***tuberculosis***	45.9	71.4	294	
	mutator mutT protein ((7,8-dihydro-				
	H37Rv MLCB637.35c				
	8-oxoguanine-triphosphatase)(8-				
	oxo-dGTPase)(dGTP				
	pyrophosphohydrolase)				
1456	4956 1383930 1384085	156			
1457	4957 1384130 1385125	996. . . 1411119	306		
1491	4991 1412000 1411437	564			
1492	4992 1412351 1412572	222			
1493	4993 1412916 1412626	291			
1494	4994 1413745 1416459	2715	sp:DPO1_MYCTU		
	Mycobacterium ***tuberculosis***	56.3	80.8	896	
	DNA polymerase I				
	polA				

1495	4995	1417883	1416462	1422	sp:CMCT_NOCLA
		Streptomyces lactamdurans	33.8	67.8	456
		cephamycin export protein			
DET D					
1561	5061	1487238	1488056	819	sp:YQXC_BACSU
		Bacillus subtilis yqxC	38.5	69.6	260
		hypothetical protein			
1562	5062	1488146	1489018	873	sp:YFJB_HAEIN
		Mycobacterium ***tuberculosis***	31.6	31.6	225
		hypothetical protein			
		H37Rv Rv1695			
1563	5063	1489103	1490881	1779	sp:RECN_ECOLI
		Escherichia coli K12 recN	31.4	63.4	574
		DNA repair protein			
1564	5064	1490944	1492134	1191	pir:H70502
		Mycobacterium ***tuberculosis***	41.9	73.1	394
		hypothetical protein			
		H37Rv Rv1697			
1565	5065	1492147	1493109	963	pir:A70503
		Mycobacterium ***tuberculosis***	30.4	68.1	313
		hypothetical protein			
		H37Rv Rv1698			
1566	5066	1493513	1495174	1662	sp:PYRG_ECOLI
		Escherichia coli K12 pyrG	55.0	76.7	549
		CTP. . . 42.8 74.0 435			GTP binding protein
1578	5078	1507327	1506662	666	
1579	5079	1507902	1507405	498	
1580	5080	1508729	1507917	813	sp:YX42_MYCTU
		Mycobacterium ***tuberculosis***	36.2	67.2	232
		methyltransferase			
		Rv3342			
1581	5081	1508813	1510366	1554	prf:2513302B
		Corynebacterium striatum M82B	29.7	60.1	499
		ABC transporter			
		tetA			
1582	5082. . . 5092	1519601	1520029	429	
		gp:AF173844_2			
		Mycobacterium smegmatis garA	75.8	93.2	
		132 signal transduction protein			
1593	5093	1520190	1520945	756	sp:Y0DF_MYCTU
		Mycobacterium ***tuberculosis***	41.9	74.4	234
		hypothetical protein			
		H37Rv Rv1828			
1594	5094	1520957	1521589	633	sp:Y0DE_MYCTU
		Mycobacterium ***tuberculosis***	30.8	63.2	133
		hypothetical protein			
		H37Rv Rv1828			
1595	5095	1521771	1522343	573	sp:Y0DE_MYCTU
		Mycobacterium ***tuberculosis***	71.4	84.3	178
		hypothetical protein			
		H37Rv Rv1828			
1596	5096	1522941	1522432	510	
1597	5097	1524500	1523052	1449	
1598	5098	1525374	1525973	600	
1599	5099. . . 1529330	1527987	1344	gp:THERAGEN_1	
		Thermus thermophilus herA	41.2	69.5	374
		DEAD box RNA helicase			
1604	5104	1529486	1530220	735	sp:YD48_MYCTU
		Mycobacterium ***tuberculosis***	34.3	66.1	245
		ABC transporter ATP-binding protein			
		H37Rv Rv1348			

1605	5105	1531816	1530341	1476	gsp:W27613	
	Brevibacterium flavum			99.0	99.2	492
	6-phosphogluconate dehydrogenase					
1606	5106	1531933	1532394	462	pir:G70664	
	Mycobacterium ***tuberculosis***			39.7	67.8	121
	thioesterase					
	H37Rv Rv1847					
1607	5107	1532322	1532996	675		
1608	5108	1533041	1533781	741	sp:NODI_RHIS3	
	Rhizobium sp. N33 nodI			39.6	68.1	235
	nodulation ATP-binding protein I					
1609	5109	1533781	1534521	741	pir:E70501	
	Mycobacterium ***tuberculosis***			43.1	76.3	232
	hypothetical membrane protein					
	H37Rv Rv1686c					
1610	5110	1535401	1534529	873	sp:YFHH_ECOLI	
	Escherichia coli K12 yfhH			26.7	63.9	277. . .
DETD . . .	5118	1542922	1542119	804	sp:THIM_SALTY	
	Salmonella typhimurium LT2			46.6	77.5	249
	hydroxyethylthiazole kinase					
	thiM					
1619	5119	1544976	1546289	1314	pir:H70830	
	Mycobacterium ***tuberculosis***			28.6	55.0	451
	cyclopropane-fatty-acyl-phospholipid					
	H37Rv ufaA1					
	synthase					
1620	5120	1547692	1546307	1386	prf:2223339B	
	Burkholderia cepacia Pc701			32.5	66.9	468
	sugar transporter. . . 1554070 615					
1629	5129	1554861	1555067	207		
1630	5130	1555079	1554891	189		
1631	5131	1555835	1555086	750		
1632	5132	1556376	1556771	396	pir:A70945	
	Mycobacterium ***tuberculosis***			71.8	87.3	110
	hypothetical protein					
	H37Rv Rv2050					
1633	5133	1557823	1557014	810	prf:2317468A	
	Schizosaccharomyces pombe			39.2	71.0	217
	dolichol phosphate mannose					
. . .	5136	1561660	1560437	1224	gp:AF188894_1	
	Candida albicans lip 1			23.7	55.6	392
	secretory lipase					
1637	5137	1561780	1562553	774	pir:C70764	
	Mycobacterium ***tuberculosis***			31.3	56.7	291
	precorrin 2 methyltransferase					
	H37Rv cobG					
1638	5138	1563802	1562525	1278	sp:COBL_PSEDE	
	Pseudomonas denitrificans			32.4	60.8	411
	precorrin-6Y C5, 15-					
	SC510 cobL					
	methyltransferase					
1639	5139	1563872	1564237	366		
1640	5140	1564237	1564482	246		
1641	5141	1565302	1564565	738	sp:YY12_MYCTU	
	Mycobacterium ***tuberculosis***			54.1	75.4	244
	oxidoreductase					
	H37Rv RV3412					
1642	5142	1566438	1565302	1137	gp:AF014460_1	
	Streptococcus mutans LT11			36.1	61.3	382
	dipeptidase or X-Pro. . . protein					
1646	5146	1571382	1571068	315	sp:YY34_MYCLE	

	Mycobacterium leprae	44.7	69.4	85	
	hypothetical protein				
	MLCB2533.27				
1647	5147 1572486 1571506	981	sp:YY35_MYCTU		
	Mycobacterium ***tuberculosis***	31.9	61.2	317	
	hypothetical protein				
	H37Rv Rv2095c				
1648	5148 1573463 1572492	972	sp:YY36_MYCLE		
	Mycobacterium leprae	32.4	64.8	324	
	hypothetical protein				
	MLCB2533.25				
1649	5149 1574915 1573491	1425	sp:YY37_MYCTU		
	Mycobacterium ***tuberculosis***	53.1	77.3	467	
	hypothetical protein				
	H37Rv Rv2097c				
1650	5150 1574957 1575205	249			
1651	5151 1575136 1574945	192	pir:B70512		
	Mycobacterium ***tuberculosis***	54.1	80.3	61	
	hypothetical protein				
	H37Rv Rv2111c				
1652	5152 1576947 1575406	1542	pir:C70512		
	Mycobacterium ***tuberculosis***	48.6	74.2	516	
	hypothetical protein				
	H37Rv Rv2112c				
1653	5153 1577327 1577806	480	PIR:H72504		
	Aeropyrum permix K1 APE2014	42.0	50.0	159	
	hypothetical. . . protein-beta-aspartate				
	methyltransferase				
1656	5156 1580771 1579449	1323	gp:AF005050_1		
	Homo sapiens	38.1	67.2	436	
	aspartyl aminopeptidase				
1657	5157 1580807 1581640	834	pir:B70513		
	Mycobacterium ***tuberculosis***	45.4	71.4	269	
	hypothetical protein				
	H37Rv Rv2119				
1658	5158 1581851 1582114	264	sp:VAPI_BACNO		
	Dichelobacter nodosus A198	40.6	72.5	69	
	virulence-associated protein				
	1594532 1594951 420	sp:ARSC_STAAU			
	Staphylococcus aureus plasmid	32.6	64.3	129	
	arsenate reductase				
	p1258 arsC				
1668	5168 1595030 1595668	639	pir:G70964		
	Mycobacterium ***tuberculosis***	47.2	75.6	123	
	arsenate reductase				
	H37Rv arsC				
1669	5169 1596221 1595844	378			
1670	5170 1597460 1596249	1212	sp:SYC_ECOLI		
	Escherichia coli K12 cysS. . . resistance protein				
1672	5172 1598667 1599614	948	prf.2214302F		
	Agrobacterium tumefaciens	33.4	62.6	326	
	oxidoreductase				
	mocA				
1673	5173 1599679 1600677	999	pir:F70577		
	Mycobacterium ***tuberculosis***	27.0	53.5	359	
	lipoprotein				
	H37Rv lppL				
1674	5174 1600692 1601804	1113	sp:PYRD_AGRAE		
	Agrocye aegerita ura 1	44.0	67.1	334	
	dihydroorotate dehydrogenase				

1675.	..	1614451	1848	sp:MUTA_STRCM	Streptomyces
		cinnamensis	41.6	68.2	610
		methylmalonyl-CoA mutase beta			
		A3823.5 mutA			
		subunit			
1690	5190	1616578	1617300	723	sp:YS13_MYCTU
		Mycobacterium	***tuberculosis***	39.7	70.1 224
		hypothetical membrane protein			
		H37Rv Rv1491c			
1691	5191	1617398	1617994	597	
1692	5192	1619616	1618321	1296	sp:YS09_MYCTU
		Mycobacterium	***tuberculosis***	64.1	87.0 370
		hypothetical membrane protein			
		H37Rv Rv1488			
1693	5193	1620106	1619672	435	pir:B70711
		Mycobacterium	***tuberculosis***	44.7	78.7 141
		hypothetical membrane protein			
		H37Rv Rv1487			
1694	5194	1621009	1620167	843	gp:SCC77_24
		Streptomyces coelicolor A3(2) 51.0 72.8 261			
		hypothetical.	..	1624826	1623027 1800
		sp:P54_ENTFC			
		Streptococcus faecium	25.5	56.5	611
		invasin			
1698	5198	1625925	1625428	498	
1699	5199	1626279	1629107	2829	pir:F70873
		Mycobacterium	***tuberculosis***	69.9	85.9 959
		aconitate hydratase			
		H37Rv acn			
1700	5200	1629298	1629861	564	pir:E70873
		Mycobacterium	***tuberculosis***	54.6	81.6 174
		transcriptional regulator			
		H37Rv Rv1474c			
1701	5201	1629913	1630668	756	pir:F64496
		Methanococcus jannaschii	21.3	51.9	235
		GMP synthetase			
		MJ1575. . .			
DETD		..	1649367	756	gp:SCC22_4
		Streptomyces coelicolor A3(2) 70.2 89.3 252			
		ABC transporter ATP-binding protein			
		SCC22.04c			
1729	5229	1651424	1650249	1176	pir:A70872
		Mycobacterium	***tuberculosis***	55.2	83.0 377
		hypothetical protein			
		H37Rv Rv1462			
1730	5230	1652875	1651433	1443	sp:Y074_SYNY3
		Synechocystis sp. PCC6803 41.0 73.0 493			
		ABC transporter			
..	5231	1653586	1652894	693	gp:SCC22_8
		Streptomyces coelicolor A3(2) 46.1 71.4 217			
		DNA-binding protein			
		SCC22.08c			
1732	5232	1654043	1655671	1629	pir:F70871
		Mycobacterium	***tuberculosis***	36.3	67.8 518
		hypothetical membrane protein			
		H37Rv Rv1459c			
1733	5233	1655681	1656700	1020	pir:S72783
		Mycobacterium leprae	50.2	77.3	317
		ABC transporter			
..		abc2			
1734	5234	1656712	1657515	804	pir:S72778
		Mycobacterium leprae	41.0	74.8	266

hypothetical protein
 MLCL536.32
 1735 5235 1657677 1658675 999 pir:C70871
 Mycobacterium ***tuberculosis*** 43.0 74.6 291
 hypothetical protein
 H37Rv Rv1456c
 1736 5236 1659496 1659140 357
 1737 5237 1659508 1661136 1629 pir:C71156
 Pyrococcus horikoshii PH0450 23.4 . . 1666601 1164
 1743 5243 1667950 1669401 1452 gsp:W27612
 Brevibacterium flavum 99.8 100.0 484
 glucose-6-phosphate

 dehydrogenase
 1744 5244 1669419 1670375 957 pir:A70917
 Mycobacterium ***tuberculosis*** 40.6 71.7 318
 oxppcycle protein (glucose 6-
 H37Rv Rv1446c opcA
 phosphate dehydrogenase

 assembly protein)
 1745 5245 1670395 1671099 705 sp:SOL3_YEAST
 Saccharomyces. . . 1682624 1002 sp:G3P_CORGL
 Corynebacterium glutamicum 99.1 99.7 333
 glyceraldehyde-3-phosphate
 AS019 ATCC 13059 gap
 dehydrogenase
 1756 5256 1685097 1684117 981 pir:D70903
 Mycobacterium ***tuberculosis*** 63.9 87.4 324
 hypothetical protein
 H37Rv Rv1423
 1757 5257 1686132 1685110 1023 sp:YR4O_MYCTU
 Mycobacterium ***tuberculosis*** 56.3 82.5 309
 hypothetical protein
 H37Rv Rv1422
 1758 5258 1687078 1686152 927 sp:YR39_MYCTU
 Mycobacterium ***tuberculosis*** 52.0 76.2 281
 hypothetical protein
 H37Rv Rv1421
 1759 5259 1689190 1687103 2088 sp:UVRC_PSEFL
 Synechocystis sp. PCC6803 34.4 61.5 701
 excinuclease ABC subunit C
 uvrC
 1760 5260 1689779 1689201 579 sp:YR35_MYCTU
 Mycobacterium ***tuberculosis*** 32.7 68.7 150
 hypothetical protein
 H37Rv Rv1417
 1761 5261 1690345 1689869 477 sp:RISB_ECOLI
 Escherichia coli K12 43.5 72.1 154
 6,7-dimethyl-8-ribityllumazine

 synthase
 1762. . . 1691012 1691347 336 GSP:Y83273
 Bacillus subtilis 44.0 52.0 106
 polypeptide encoded by rib operon
 1765 5265 1691625 1690360 1266 gp:AF001929_1
 Mycobacterium ***tuberculosis*** ribA 65.6 84.7 404
 GTP cyclohydrolase II and 3,4-

 dihydroxy-2-butanone 4-phosphate

	synthase (riboflavin synthesis)				
1766	5266	1692271	1691639	633	sp:RISA_ACTPL
	Actinobacillus. . . n				
1773	5273	1700397	1699177	1221	gsp:R80060
	Brevibacterium flavum MJ-233				99.3 99.5 407
	S-adenosylmethionine synthetase				
1774	5274	1701767	1700508	1260	sp:DFP_MYCTU
	Mycobacterium ***tuberculosis***				58.0 80.9 409
	DNA/pantothenate metabolism				
	H37Rv RV1391 dfp				
	flavoprotein				
1775	5275	1702322	1702032	291	sp:YD90_MYCTU
	Mycobacterium ***tuberculosis***				70.4 87.7 81
	hypothetical protein				
	H37Rv Rv1390				
1776	5276	1703037	1702411	627	pir:KIBYGU
	Saccharomyces cerevisiae guk1				39.8 74.7 186
	guanylate kinase				
1777	5277	1703308	1702991	318	pir:B70899
	Mycobacterium ***tuberculosis***				80.6 90.3 103
	integration host factor				
	H37Rv Rv1388 mlHF				
1778	5278	1704350	1703517	834	sp:DCOP_MYCTU
	Mycobacterium ***tuberculosis***				51.8 73.6 276
	orotidine-5'-phosphate				
	H37Rv uraA				
	decarboxylase				
1779	5279	1707697	1704359	3339	pir:SYECCP
	Escherichia coli carB				53.1 77.5 1122
	carbamoyl-phosphate synthase				
	. . . caldolyticus DSM 405				54.0 80.1 176
	phosphoribosyl transferase or				
	pyrR				
	pyrimidine operon regulatory protein				
1784	5284	1712596	1713759	1164	sp:Y00R_MYCTU
	Mycobacterium ***tuberculosis***				39.7 73.4 297
	cell division inhibitor				
	H37Rv Rv2216				
1785	5285	1713830	1714306	477	
1786	5286	1714299	1714760	462	
1787	5287	1714741	1714950	210	
1788	. . . 1724578	753			sp:FHUC_BACSU Bacillus subtilis
	168 fhuC				38.3 71.7 230 ferrichrome
	transport ATP-binding				
	protein				
1799	5299	1725439	1724612	828	pir:D70660
	Mycobacterium ***tuberculosis***				50.0 60.0 259
	shikimate 5-dehydrogenase				
	H37Rv aroE				
1800	5300	1726625	1725459	1167	pir:E70660
	Mycobacterium ***tuberculosis***				41.8 70.1 395
	hypothetical protein				
	H37Rv Rv2553c				
1801	5301	1727170	1726625	546	pir:F70660
	Mycobacterium ***tuberculosis***				52.8 69.6 161
	hypothetical protein				
	H37Rv Rv2554c				
1802	5302	1730048	1727385	2664	sp:SYA_THIFE
	Thiobacillus ferrooxidans ATCC				43.3 71.8 894
	alanyl-tRNA synthetase				

33020 alaS

1803 5303 1731542 1730166 1377 sp:Y0A9_MYCTU
Mycobacterium ***tuberculosis*** 65.4 84.8 454
hypothetical protein
H37Rv Rv2559c

1804 5304 1732822 1731599 1224

1805 5305 1734811 1732988 1824 sp:SYD_MYCLE
Mycobacterium leprae aspS 71.1 89.2 591
aspartyl-tRNA synthetase

1806 5306 1735056 1735946 891 sp:Y0BQ_MYCTU
Mycobacterium ***tuberculosis*** 46.1 74.1 297
hypothetical protein
H37Rv Rv2575

1807 5307 1738679 1736004 2676 sp:AMYPH_YEAST
Saccharomyces cerevisiae 26.1 53.6 839
glucan 1,4-alpha-glucosidase
S288C. . .

DET D . . . 1755599 150 gp:AF038651_1
Corynebacterium glutamicum 98.0 98.8 49
dipeptide transport system
ATCC 13032 dcIAE

1827 5327 1757228 1755486 1743 sp:Y0BG_MYCTU
Mycobacterium ***tuberculosis*** 30.7 60.9 558
hypothetical protein
H37Rv Rv2585c

1828 5328 1758797 1757589 1209 sp:SECF_ECOLI
Escherichia coli K12 secF 25.9 57.2 332
protein-export. . . 5337 1765969 1766442 474
gp:SC10A5_9 Streptomyces coelicolor A3(2) 31.5 61.3
111 hypothetical protein
SC10A5.09c

1838 5338 1766948 1766487 462 pir:H70570
Mycobacterium ***tuberculosis*** 38.2 61.2 170
hypothetical protein
H37Rv Rv2609c

1839 5339 1768030 1766948 1083 sp:GPI3_YEAST
Saccharomyces cerevisiae 21.7 49.3 414
hexosyltransferase or N-
. . . protein

1840 5340 1768996 1768034 963 gp:SCL2_16
Streptomyces coelicolor A3(2) 46.4 67.8 295
acyltransferase
SCL2.16c

1841 5341 1769678 1769022 657 pir:C70571
Mycobacterium ***tuberculosis*** 48.2 78.0 78
CDP-diacylglycerol-glycerol-3-
H37Rv Rv2612c pgsA
phosphate phosphatidyltransferase

1842 5342 1770340 1769681 660 pir:D70571
Mycobacterium ***tuberculosis*** 54.6 78.4 194
histidine triad (HIT) family protein
H37Rv Rv2613c

1843 5343 1772384 1770327 2058 sp:SYT2_BACSU
Bacillus subtilis thrZ 42.0 68.9 . . . 1928908
375

2000 5500 1930879 1929059 1821

2001 5501 1931190 1930990 201

2002 5502 1931888 1931421 468

2003 5503 1932315 1931935 381 pir:H70638
Mycobacterium ***tuberculosis*** 38.6 58.8 114
hypothetical protein

H37Rv Rv1956						
2004	5504	1932879	1932373	507		
2005	5505	1934358	1933522	837		
2006	5506	1935912	1934971	942	sp:Y137_METJA.	
DETD						
	yxmA	48.9	81.5	92	hypothetical	
	protein					
2081	5581	1996768	1997112	345		
2082	5582	1997168	1997503	336		
2083	5583	1997545	1998240	696	pir:C70968	
	Mycobacterium ***tuberculosis***	33.5	64.4	233		
	riboflavin biosynthesis protein					
	H37Rv Rv2671 ribD					
2084	5584	1998289	1999542	1254	pir:E70968	
	Mycobacterium ***tuberculosis***	42.5	71.9	384		
	potential membrane protein					
	H37Rv Rv2673					
2085	5585	1999542	1999949	408	gp:AF128264_2	
	Streptococcus gordonii msrA	41.3	67.5	126		
	methionine sulfoxide reductase					
2086	5586	2000132	1999707	426		
2087	5587	2001216	2000521	696	pir:H70968	
	Mycobacterium ***tuberculosis***	55.2	77.2	232		
	hypothetical protein					
	H37Rv Rv2676c					
2088	5588	2001489	2002112	624	pir:C70528	
	Mycobacterium ***tuberculosis***	55.7	78.6	201		
	hypothetical protein					
	H37Rv Rv2680					
2089	5589	2002072	2003334	1263	sp:RND_HAEIN	
	Haemophilus influenzae Rd	25.9	52.8	371		
	ribonuclease D					
	pir:E72298	Thermotoga maritima MSB8		25.4		
	52.3	472	RNA methyltransferase			
	TM1094					
2092	5592	2006698	2006979	282		
2093	5593	2007637	2006777	861	pir:C70530	
	Mycobacterium ***tuberculosis***	38.1	62.7	268		
	hypothetical protein					
	H37Rv Rv2696c					
2094	5594	2008184	2007738	447	sp:DUT_STRCO	
	Streptomyces coelicolor A3(2)	55.0	82.1	140		
	deoxyuridine 5'-triphosphate					
	SC2E9.09 dut					
	nucleotidohydrolase					
2095	5595	2008250	2008798	549	pir:E70530	
	Mycobacterium ***tuberculosis***	46.0	70.7	150		
	hypothetical protein					
	H37Rv Rv2698					
2096	5596	2009082	2008876	207		
2097	5597	2009570	2009280	291	pir:F70530	
	Mycobacterium ***tuberculosis***	58.0	81.0	100		
	hypothetical protein					
	H37Rv Rv2699c					
2098	5598	2010539	2009724	816	sp:SUHB_ECOLI	
	Escherichia coli k12 suhB	38.4	68.2	198		
	extragenic suppressor protein					
2099	5599	2010555	2011382	828	sp:PPGK_MYCTU	
	Mycobacterium ***tuberculosis***	54.4	80.2	248		
	polyphosphate glucokinase					

H37Rv RV2702 ppgK

2100	5600	2011863	2013356	1494	prf:2204286A
		Corynebacterium glutamicum	98.0	98.6	500
		sigma factor. . . sp:YRKO_BACSU			Bacillus subtilis yrkO
		23.9	51.4	422	hypothetical membrane protein

2102	5602	2016121	2015585	537	
2103	5603	2017966	2016257	1710	sp:Y065_MYCTU
		Mycobacterium ***tuberculosis***	61.3	80.8	578
		hypothetical protein			

H37Rv Rv2917

2104	5604	2018119	2018754	636	pir:H70531
		Mycobacterium ***tuberculosis***	32.3	59.1	127
		hypothetical membrane protein			

H37Rv Rv2709

2105	5605	2018202	2017966	237	pir:G70531
		Mycobacterium ***tuberculosis***	65.8	85.5	76
		hypothetical protein			

H37Rv Rv2708c

2106	5606	2018744	2020276	1533	gp:SCH5_8
		Streptomyces coelicolor A3(2)	33.5	61.2	523
		transferase			
		SCH5.08c			

2107. . . 99.1 99.1 329 UDP-glucose 4-epimerase

ATCC 13869 (Brevibacterium lactofermentum) galE

2111	5611	2025270	2023948	1323	
2112	5612	2025423	2026379	957	pir:E70532
		Mycobacterium ***tuberculosis***	45.3	79.0	305
		hypothetical protein			

H37Rv Rv2714

2113	5613	2026494	2029043	2550	sp:MTR4_YEAST
		Saccharomyces cerevisiae	24.4	50.7	661
		ATP-dependent RNA helicase			

. . . coli K12 miaA 40.0 68.7 300 tRNA

delta-2-

isopentenylpyrophosphate

transferase

2134	5634	2054283	2053609	675	
2135	5635	2054403	2055761	1359	pir:B70506
		Mycobacterium ***tuberculosis***	48.5	75.7	445
		hypothetical protein			

H37Rv Rv2731

2136	5636	2055743	2054724	1020	
2137	5637	2055765	2056787	1023	
2138	5638	2057788	2057120	669	pir:C70506
		Mycobacterium ***tuberculosis***	29.0	63.7	190
		hypothetical membrane protein			

H37Rv Rv2732c

2139	5639	2059420	2057855	1566	sp:Y195_MYCLE
		Mycobacterium leprae	68.4	86.4	494
		hypothetical protein			

. . . gluD

2144	5644	2063894	2063298	597	sp:RECX_MYCLE
		Mycobacterium leprae recX	34.5	66.9	142
		regulatory protein			

2145	5645	2065627	2065394	234	pir:A70878
		Mycobacterium ***tuberculosis***	40.3	71.6	67
		hypothetical protein			

H37Rv Rv2738c

2146	5646	2066404	2065667	738	
2147	5647	2066566	2067141	576	sp:BIOY_BACSH
		Bacillus sphaericus bioY	33.0	5649	2067866
	2068474	609	pir:F69742		Bacillus subtilis ybaF
	24.6	58.8	228		hypothetical membrane protein
2150	5650	2068703	2069392	690	pir:B60176
		Mycobacterium ***tuberculosis***	41.7	78.5	228
		hypothetical protein			
2151	5651	2069383	2068556	828	sp:35KD_MYCTU
		Mycobacterium ***tuberculosis***	72.5	89.6	269
		hypothetical protein (35kD protein)			
		H37Rv RV2744C			
2152	5652	2069936	2069616	321	pir:H70878
		Mycobacterium ***tuberculosis***	54.2	78.3	83
		regulator (DNA-binding protein)			
		H37Rv Rv2745c			
2153	5653	2070512	2069997	516	sp:CINA_STRPN
		Streptococcus pneumoniae R6X	41.8	68.5	165
		competence. . .			
DETD . . .	2089868	2089218	651		gp:SC5A7_23
		Streptomyces coelicolor A3(2)	42.2	62.5	237
		hypothetical protein			
		SC5A7.23			
2172	5672	2090664	2089861	804	pir:B70885
		Mycobacterium ***tuberculosis***	46.9	68.9	273
		phosphoesterase			
		H37Rv Rv2795c			
2173	5673	2092055	2090751	1305	pir:G70693
		Mycobacterium ***tuberculosis***	51.0	78.8	433
		DNA damaged inducible protein f			
		H37Rv Rv2836c dinF			
2174	5674	2093046	2092051	996	pir:H70693
		Mycobacterium ***tuberculosis***	36.7	70.8	308
		hypothetical protein			
		H37Rv Rv2837c			
2175	5675	2093501	2093055	447	sp:RBFA_BACSU
		Bacillus subtilis 168 rbfA	32.4	70.4	108
		ribosome-binding. . .	42.3	71.0	352
		n-utilization substance protein			

(transcriptional

termination/antitermination factor)

2179	5679	2098562	2099815	1254	
2180	5680	2098945	2098412	534	pir:E70588
		Mycobacterium ***tuberculosis***	34.6	65.5	165
		hypothetical protein			
		H37Rv Rv2842c			
2181	5681	2100240	2101841	1602	sp:DPPE_BACSU
		Bacillus subtilis 168 dppE	25.3	60.9	534
		peptide-binding. . .			permease
2183	5683	2102975	2103973	999	prf:1709239C
		Bacillus subtilis spo0KC	38.4	69.2	292
		oligopeptide permease			
2184	5684	2103973	2105703	1731	pir:H70788
		Mycobacterium ***tuberculosis***	57.6	81.3	552
		peptidetransport system ABC-			
		H37Rv Rv3663c dppD			
		transporter ATP-binding protein			
2185	5685	2107564	2105801	1764	sp:SYP_MYCTU
		Mycobacterium ***tuberculosis***	67.0	84.6	578

prolyl-tRNA synthetase
 H37Rv Rv2845c proS
 2186 5686 2107652 2108386 735 gp:SCC30_5
 Streptomyces coelicolor A3(2) 39.5 65.0 243
 hypothetical. . . 2113616 2112717 900 gp:SC5H1_10
 Streptomyces coelicolor A3(2) 35.1 62.3 151
 hypothetical protein
 SC5H1.10c
 2192 5692 2115761 2116774 1014 pir:A70590
 Mycobacterium ***tuberculosis*** 37.6 65.7 338
 hypothetical protein
 H37Rv Rv2854
 2193 5693 2116916 2118310 1395 sp:GSHR_BURCE
 Burkholderia cepacia AC1100 53.0 76.6 466
 glutathione reductase
 . . . coli K12 gcpE 44.3 73.8 359
 hypothetical protein (gcpE protein)
 2206 5706 2128850 2129461 612
 2207 5707 2129880 2128669 1212 pir:G70886
 Mycobacterium ***tuberculosis*** 43.0 73.6 405
 hypothetical membrane protein
 H37Rv Rv2869c
 2208 5708 2130306 2130950 645 GSP:Y37145
 Chlamydia trachomatis 36.0 43.0 147
 polypeptides can. . . 2133406 855 pir:B72334
 Thermotoga maritima MSB8 37.1 75.1 245
 ABC transporter ATP-binding protein
 TM0793
 2214 5714 2135551 2134454 1098 sp:YS80_MYCTU
 Mycobacterium ***tuberculosis*** 66.0 78.0 356
 pyruvate formate-lyase 1 activating
 H37Rv
 enzyme
 2215 5715 2135884 2136141 258 pir:A70801
 Mycobacterium ***tuberculosis*** 41.5 74.5 94
 hypothetical membrane protein
 H37Rv Rv3760
 2216 5716 2137089 2136235 855 sp:CDSA_PSEAE
 Pseudomonas aeruginosa 33.3 56.5 294
 phosphatidate cytidyltransferase
 . . . 2140886 2140071 816 pir:A69699 Bacillus
 subtilis rpsB 54.7 83.5 254 30S
 ribosomal protein S2
 2222 5722 2141257 2141760 504 sp:YS91_MYCTU
 Mycobacterium ***tuberculosis*** 46.0 58.0 120
 hypothetical protein
 H37Rv Rv2891
 2223 5723 2142686 2141763 924 prf:2417318A
 Proteus mirabilis xerD 40.1 68.7 297
 site-specific recombinase
 2224 5724 2144066 2142885 1182 sp:YX27_MYCTU
 Mycobacterium ***tuberculosis*** 39.8 66.8 395
 hypothetical protein
 H37Rv Rv2896c
 2225 5725 2145586 2144066 1521 sp:YX28_MYCTU
 Mycobacterium ***tuberculosis*** 46.6 75.8 504
 Mg(2+) chelatase family protein
 H37Rv Rv2897c
 2226 5726 2145941 2145576 366 sp:YX29_MYCTU
 Mycobacterium ***tuberculosis*** 40.3 72.3 119
 hypothetical protein

H37Rv Rv2898c
2227 5727 2146566 2146264 303 sp:YT01_MYCTU
Mycobacterium ***tuberculosis*** 68.3 96.0 101
hypothetical protein
H37Rv Rv2901c
2228 5728 2147192 2146566 627 sp:RNH2_HAEIN
Haemophilus influenzae Rd 42.6 69.5 190
ribonuclease HII
. . . 1144 glucan 1,4-alpha-glucosidase or
S288C YIR019C stal
glucoamylase S1/S2 precursor
2263 5763 2180918 2181880 963
2264 5764 2183092 2179628 3465 sp:Y06B_MYCTU
Mycobacterium ***tuberculosis*** 48.3 72.6 1206
chromosome segregation protein
H37Rv Rv2922c smc
2265
DET.D 5765 2183391 2183110 282 sp:ACYP_MYCTU
Mycobacterium ***tuberculosis*** 51.1 73.9 92
acylphosphatase
H37Rv RV2922.1C
2266 5766 2185258 2183405 1854
2267 5767 2186208 2185351 858 sp:YFER_ECOLI
Escherichia coli K12 yfeR 23.9 . . 5773 2189906
2189166 741 pir:B69693 Bacillus subtilis 168
rncS 40.3 76.5 221 ribonuclease III
2274 5774 2190439 2189906 534 sp:Y06F_MYCTU
Mycobacterium ***tuberculosis*** 35.8 62.5 176
hypothetical protein
H37Rv Rv2926c
2275 5775 2191328 2190540 789 sp:Y06G_MYCTU
Mycobacterium ***tuberculosis*** 50.0 76.9 238
hypothetical protein
H37Rv Rv2927c
2276 5776 2191522 2193165 1644 prf:2104260G
Streptomyces verticillus 28.3 55.6 559
transport protein
2277 5777 . . . 2208367 801 sp:TRPG_EMENI
Emericella nidulans trpC 29.6 62.1 169
indole-3-glycerol-phosphate

synthase/anthranilate synthase

component II

2289 5789 2209888 2209232 657 pir:H70556
Mycobacterium ***tuberculosis*** 29.4 58.8 228
hypothetical membrane protein
H37Rv Rv1610
2290 5790 2210273 2209920 354 sp:HIS3_RHOSH
Rhodobacter sphaeroides ATCC 52.8 79.8 89
phosphoribosyl-AMP. . . 5805 2222528 2225035 2508
prf:2307203B Sulfolobus acidocaldarius treX 47.4 75.5
722 glycogen debranching enzyme
2306 5806 2225149 2225949 801 pir:E70572
Mycobacterium ***tuberculosis*** 50.0 76.0 258
hypothetical protein
H37Rv Rv2622
2307 5807 2226763 2225990 774 gp:SC2G5_27
Streptomyces coelicolor A3(2) 29.9 55.2 268
oxidoreductase
SC2G5.27c. . . 1066 isoleucyl-tRNA synthetase

A364A YBL076C ILS1

2353	5853	2274688	2274473	216	
2354	5854	2275861	2274767	1095	
2355	5855	2276637	2276353	285	pir:F70578
	Mycobacterium	***tuberculosis***		46.3	73.2 82
	hypothetical membrane protein				
	H37Rv Rv2146c				
2356	5856	2277336	2276881	456	gp:BLFTSZ_6
	Brevibacterium lactofermentum		99.3	99.3	152
	hypothetical protein. . .				
DETD					
	. . .	1953	pir:S54872	Pseudomonas aeruginosa pbpB	
	28.2	58.8	650	penicillin-binding protein	
2373	5873	2294117	2293323	795	
2374	5874	2295127	2294117	1011	pir:A70581
	Mycobacterium	***tuberculosis***		55.1	79.3 323
	hypothetical protein				
	H37Rv Rv2165c				
2375	5875	2295804	2295376	429	gp:MLCB268_11
	Mycobacterium leprae		72.0	88.8	143
	hypothetical membrane protein				
	MLCB268.11c				
2376	5876	2296898	2296512	387	pir:C70935
	Mycobacterium	***tuberculosis***		39.4	69.3 137
	hypothetical protein				
	H37Rv Rv2169c				
2377	5877	2297653	2297231	423	
2378	5878	2297866	2298438	573	gp:MLCB268_13
	Mycobacterium leprae		36.3	65.3. . .	gp:MLCB268_16
	Mycobacterium leprae		35.7	69.6	484
	hypothetical membrane protein				
	MLCB268.17				
2382	5882	2302179	2302685	507	
2383	5883	2302619	2302251	369	pir:A70936
	Mycobacterium	***tuberculosis***		43.2	68.8 125
	hypothetical protein				
	H37Rv Rv2175c				
2384	5884	2302833	2304980	2148	gp:AB019394_1
	Streptomyces coelicolor A3(2)		34.2	62.4	684
	eukaryotic-type protain. . .				
		5886	2304983	2306218	
	1236	gp:MLCB268_21	Mycobacterium leprae		
	30.7	58.4	411	hypothetical membrane protein	
	MLCB268.23				
2387	5887	2306314	2307621	1308	pir:G70936
	Mycobacterium	***tuberculosis***		30.4	62.0 434
	hypothetical membrane protein				
	H37Rv ***Rv2181***				
2388	5888	2309082	2307697	1386	gp:AF260581_2
	Amycolatopsis mediterranei		66.9	87.9	462
	3-deoxy-D-arabino-heptulosonate-7-				
	phosphate synthase				
2389	5889	2309676	2309173	504	gp:MLCB268_20
	Mycobacterium leprae		58.4	77.7	166
	hypothetical protein				
	MLCB268 21c				
2390	5890	2309835	2312252	2418	pir:G70936
	Mycobacterium	***tuberculosis***		35.1	64.5 428
	hypothetical membrane protein				
	H37Rv ***Rv2181***				
2391	5891	2312360	2313808	1449	sp:CSP1_CORGL

Corynebacterium glutamicum	28.2	57.1	440	
major secreted protein PS1 protein				
(Brevibacterium flavum) ATCC				
precursor				
17965. . . qcrA	37.9	57.1	203	
ubiquinol-cytochrome c reductase				
iron-sulfur subunit (Rieske [eFe-2S])				
iron-sulfur protein cyoB				
2401 5901 2325195 2324311	885		sp:Y005_MYCTU	
Mycobacterium ***tuberculosis***	58.6	83.1	278	
ubiquinol-cytochrome c reductase				
H37Rv Rv2194 qcrC				
cytochrome c				
2402 5902 2325887 2325273	615		sp:COX3_SYNVU	
Synechococcus vulcanus	36.7	70.7	188	
cytochrome c oxidase subunit III				
2403 5903 2326273 2326121	153			
2404 5904 2326900 2326472	429		sp:Y00A_MYCTU	
Mycobacterium ***tuberculosis***	38.6	71.0	145	
hypothetical membrane protein				
H37Rv Rv2199c				
2405 5905 2327997 2326921	1077		sp:COX2_RHOSH	
Rhodobacter sphaeroides ctaC	28.7	53.9	317	
cytochrome. . . 1044			sp:LIPA_PELCA	
carbinolicus GRA BD	44.6	70.9	285	
lipA				
synthetase				
2421 5921 2343479 2344258	780		sp:Y00U_MYCTU	
Mycobacterium ***tuberculosis***	45.5	76.7	257	
hypothetical membrane protein				
H37Rv Rv2219				
2422 5922 2344431 2346047	1617		sp:YIDE_ECOLI	
Escherichia coli K12 yidE	32.9	67.8	559. . . 5943	
2364352 2365455 1104			gp:SCE9_39	
Streptomyces coelicolor A3(2)	26.8	54.1	392	
hypothetical protein				
SCE9.39c				
2444 5944 2365587 2367413	1827		sp:Y017_MYCTU	
Mycobacterium ***tuberculosis***	33.4	58.2	601	
hypothetical protein				
H37Rv Rv2226				
2445 5945 2367652 2367473	180		gp:SCC75A_11	
Streptomyces coelicolor A3(2)	38.9	55.6	54	
hypothetical protein				
. . . 1266 gp:AF174645_1			Brucella abortus vacB	
27.1 54.5 358			virulence-associated protein	
2448 5948 2370423 2370908	486			
2449 5949 2372557 2371412	1146		sp:Y019_MYCTU	
Mycobacterium ***tuberculosis***	54.7	75.1	382	
bifunctional protein (ribonuclease H				
H37Rv Rv2228c				
and phosphoglycerate mutase)				
2450 5950 2372561 2373289	729			
2451 5951 2373289 2372573	717		sp:Y01A_MYCTU	
Mycobacterium ***tuberculosis***	26.5	58.6	249	
hypothetical protein				
H37Rv Rv2229c				
2452 5952 2374462 2373323	1140		sp:Y01B_MYCTU	
Mycobacterium ***tuberculosis***	49.2	76.2	378	

hypothetical protein
 H37Rv Rv2230c
 2453 5953 2374544 2375197 654 sp:GPH_ECOLI
 Escherichia coli K12 gph 26.0 54.4 204
 phosphoglycolate. . . sp:PTPA_STRCO Streptomyces coelicolor
 A3(2) 46.2 63.5 156 low molecular weight
 protein-
 SCQ11.04c ptpA
 tyrosine-phosphatase
 2455 5955 2375767 2376720 954 sp:Y01G_MYCTU
 Mycobacterium ***tuberculosis*** 40.9 65.5 281
 hypothetical protein
 H37Rv Rv2235
 2456 5956 2377390 2376998 393 sp:YI21_BURCE
 Burkholderia cepacia 32.6 56.6 129
 insertion element (IS402)
 2457. . . gp:SC8F4_22 Streptomyces coelicolor A3(2) 30.4
 57.8 135 transcriptional regulator
 SC8F4.22c
 2459 5959 2378292 2378489 198
 2460 5960 2379312 2378884 429 sp:Y01K_MYCTU
 Mycobacterium ***tuberculosis*** 55.2 77.6 134
 hypothetical protein
 H37Rv Rv2239c
 2461 5961 2379426 2379770 345
 2462 5962 2380033 2382744 2712 gp:AF047034_4
 Streptomyces seoulensis pdhA 55.9. . .
 DETD . . . 5983 2397264 2399099 1836
 gp:SCI51_17 Streptomyces coelicolor A3(2) 44.4 73.1
 594 hypothetical protein
 SCI51.17
 2484 5984 2399158 2399397 240 pir:G70661
 Mycobacterium ***tuberculosis*** 41.2 72.1 68
 hypothetical protein
 H37Rv Rv2342
 2485 5985 2400342 2399668 675
 2486 5986 2401303 2399405 1899 prf:2413330B
 Mycobacterium smegmatis 59.1 82.9. . .
 triphosphohydrolase
 2494 5994 2406936 2406262 675 gp:NMA1Z2491_235
 Neisseria meningitidis NMA0251 30.4 59.7 171
 hypothetical protein
 2495 5995 2406993 2409029 2037 pir:B70662
 Mycobacterium ***tuberculosis*** 31.1 63.6 692
 hypothetical protein
 H37Rv Rv2345
 2496 5996 2410264 2409779 486 gp:AE003565_26
 Drosophila melanogaster 24.6 54.4 138
 hypothetical protein
 CG10592
 2497. . . 582
 2498 5998 2412338 2410956 1383 pir:S58522
 Thermus aquaticus HB8 46.1 69.9 508
 glycyl-tRNA synthetase
 2499 5999 2412580 2412948 369 pir:E70585
 Mycobacterium ***tuberculosis*** 49.4 73.0 89
 bacterial regulatory protein, arsR
 H37Rv Rv2358 furB
 family
 2500 6000 2412992 2413423 432 sp:FUR_ECOLI
 Escherichia coli K12 fur 34.9 70.5 132

ferric uptake regulation protein

2501	6001	2413568	2415118	1551	pir:A70539
	Mycobacterium	***tuberculosis***		24.8	46.7 529
	hypothetical protein (conserved in H37Rv Rv1128c C.glutamicum?)				
2502	6002	2416089	2415298	792	gp:AF162938_1
	Streptomyces coelicolor A3(2)		40.6	67.0 . . .	2416371
	729	sp:UPPS_MICLU			Micrococcus luteus B-P 26 uppS
	43.4	71.2	233		undecaprenyl diphosphate synthase
2504	6004	2417947	2417222	726	pir:A70586
	Mycobacterium	***tuberculosis***		45.7	74.3 245
	hypothetical protein H37Rv Rv2362c				
2505	6005	2418883	2417969	915	gp:AF072811_1
	Streptococcus pneumoniae era		39.5	70.3	296
	Era-like GTP-binding protein				
2506	6006	2420309	2418990	1320	sp:Y1DE_MYCTU
	Mycobacterium	***tuberculosis***		52.8	82.4 432
	hypothetical membrane protein H37Rv Rv2366				
2507	6007	2420900	2420313	588	sp:YN67_MYCTU
	Mycobacterium	***tuberculosis***		65.0	86.0 157
	hypothetical protein H37Rv Rv2367c				
2508	6008	2420973	2421236	264	GSP:Y75650
	Neisseria meningitidis		45.0	50.0	85
	Neisserial polypeptides predicted to				
	be useful antigens for vaccines and				
	diagnostics				
2509	6009	2421949	2420900	1050	sp:PHOL_MYCTU
	Mycobacterium	***tuberculosis***		61.1	84.6 344
	phosphate starvation inducible H37Rv Rv2368c phoH protein				
2510	6010	2422697	2421975	723	gp:SCC77_19
	Streptomyces coelicolor A3(2)		44.0	75.4 . . .	68.3 690
	peptidyl-dipeptidase				
2526	6026	2436871	2438049	1179	gp:AF064523_1
	Anisopteromalus calandrae		24.1	45.7	453
	carboxylesterase				
2527	6027	2438113	2439906	1794	pir:G70983
	Mycobacterium	***tuberculosis***		65.2	84.9 594
	glycosyl hydrolase or trehalose H37Rv Rv0126 synthase				
2528	6028	2439906	2440994	1089	pir:H70983
	Mycobacterium	***tuberculosis***		32.1	58.8 449
	hypothetical protein H37Rv Rv0127				
2529	6029	2441589	2441005	585	pir:T07979
	Chlamydomonas reinhardtii ipi1		31.8	57.7	189
	isopentenyl-diphosphate Delta-				
. . .	6067	2484392	2482548	1845	sp:LEPA_BACSU
	Bacillus subtilis 168 lepA		58.7	83.6	603
	GTP-binding protein				
2568	6068	2484661	2485269	609	pir:H70683
	Mycobacterium	***tuberculosis***		41.6	69.7 185
	hypothetical protein				

H37Rv Rv2405

2569 6069 2485473 2485733 261 sp:RS20_ECOLI
 Escherichia coli K12 rps T 48.2 72.9 85. . . 6071
 2486881 2486477 405 gp:SC6D7_25
 Streptomyces coelicolor A3(2) 61.2 80.6 129
 ankyrin-like protein
 SC6D7.25.

2572 6072 2487884 2486910 975 pir:H70684
 Mycobacterium ***tuberculosis*** 46.0 74.1 313
 hypothetical protein
 H37Rv Rv2413c

2573 6073 2489450 2487912 1539 sp:CME3_BACSU
 Bacillus subtilis 168 comEC 21.4 49.7 527
 late. . . 6076 2491111 2490290 822
 gp:SCC123_7 Streptomyces coelicolor A3(2) 34.8 66.3
 273 hypothetical protein
 SCC123.07c.

2577 6077 2491858 2491151 708 pir:F70685
 Mycobacterium ***tuberculosis*** 46.8 66.4 235
 phosphoglycerate mutase
 H37Rv Rv2419c

2578 6078 2492343 2491873 471 pir:G70685
 Mycobacterium ***tuberculosis*** 55.6 86.3 117
 hypothetical protein
 H37Rv Rv2420c

2579 6079 2493178 2492501 678 gp:SCC123_17
 DETD . . . 6101 2512803 2513144 342
 gp:AE002024_10 Deinococcus radiodurans R1 34.8 67.4
 92 hypothetical protein
 DR1844

2602 6102 2513618 2513154 465 pir:H70515
 Mycobacterium ***tuberculosis*** 36.6 64.3 112
 hypothetical protein
 H37Rv Rv1883c

2603 6103 2514114 2513692 423 pir:E70863
 Mycobacterium ***tuberculosis*** 33.9 68.6 118
 hypothetical protein
 H37Rv Rv2446c

2604 6104 2515487 2514114 1374 prf:2410252B
 Streptomyces coelicolor A3(2) 55.4 79.6 451
 folyl-polyglutamate synthetase
 . . . 2541024 2540335 690 prf:2408324B
 Rhodococcus opacus pcaH 74.7 91.2 217
 protocatechuate dioxygenase beta
 subunit

2633 6133 2542350 2541187 1164 pir:G70506
 Mycobacterium ***tuberculosis*** 26.4 48.7 273
 hypothetical protein
 H37Rv Rv0336

2634 6134 2542802 2542512 291 prf:2515333B
 Mycobacterium ***tuberculosis*** 54.4 81.5 92
 muconolactone isomerase
 catC

2635 6135 2543043 2543813 771
 2636 6136 2543936 2542818 1119 sp:CATB_RHOOP
 Rhodococcus opacus 1CP catB 60.8. . . lacB

2662 6162 2565245 2564550 696 sp:YAMY_BACAD
 Bacillus acidopullulyticus ORF2 26.2 58.1 248
 hypothetical protein

2663 6163 2566231 2565623 609 pir:A70866

	Mycobacterium	***tuberculosis***	56.8	80.9	199	
	hypothetical protein					
	H37Rv	Rv2466c				
2664	6164	2566345	2568945	2601	sp:AMPN_STRLI	
	Streptomyces	lividans pepN	47.5	70.5	890	
	aminopeptidase N					
2665	2584613	2585926	1314	sp:ARGD_CORGL		
	Corynebacterium	glutamicum	31.4	63.5	411	
	acetylornithine aminotransferase					
	ATCC 13032	argD				
2682	6182	2586180	2587763	1584	pir:A70539	
	Mycobacterium	***tuberculosis***	25.1	47.9	482	
	hypothetical protein					
	H37Rv	Rv1128c				
2683	6183	2587976	2588722	747	sp:YA26_MYCTU	
	Mycobacterium	***tuberculosis***	49.1	79.4	218	
	hypothetical membrane protein					
	H37Rv	Rv0364				
2684	6184	2589432	2588725	708	sp:PHBB_CHRVI	
	Chromatium	vinosum D phbB	28.1	60.0	235	
DETD	2593965	1128	sp:CHRA_PSEAE			
	Pseudomonas	aeruginosa	27.3	60.4	396	
	chromate transport protein					
	Plasmid pUM505	chrA				
2690	6190	2594594	2593968	627	pir:A70867	
	Mycobacterium	***tuberculosis***	37.8	68.9	196	
	hypothetical protein					
	H37Rv	Rv2474c				
2691	6191	2595061	2594597	465	gp:SC6D10_19	
	Streptomyces	coelicolor A3(2)	36.2	61.4	127	
	hypothetical protein					
2596048	1668	sp:YJJK_ECOLI	Escherichia coli K12			
yjiK	52.8	79.6	563	ABC transporter		
	ATP-binding protein					
2695	6195	2598483	2597869	615	pir:E70867	
	Mycobacterium	***tuberculosis***	31.4	62.2	172	
	hypothetical protein					
	H37Rv	Rv2478c				
2696	6196	2600764	2598662	2103	sp:Y05L_MYCLE	
	Mycobacterium	leprae 0659	28.0	56.7	700	
	hypothetical membrane	6213	2617246	2617995	750	
	sp:GIP_ECOLI	Escherichia coli K12 gip	41.2	69.4		
255	glyoxylate-induced protein					
2714	6214	2618072	2618869	798	pir:E70761	
	Mycobacterium	***tuberculosis***	40.0	57.0	258	
	ketoacyl reductase					
	H37Rv	Rv1544				
2715	6215	2618882	2619538	657	sp:ORN_ECOLI	
	Escherichia coli K12	orn	48.0	78.8	179	
	oligoribonuclease					
2716	6216	2620728	2619541	1188	prf:2409378A	
	Salmonella enterica	iroD	26.0	50.9	454	
	ferric enterochelin esterase					
2717	6217	2622181	2620973	1209	pir:C70870	
	Mycobacterium	***tuberculosis***	48.5	71.9	398	
	lipoprotein					
	H37Rv	Rv2518c lppS				
2718	6218	2622961	2623605	645		
2719	6219	2623770	2623621	150		
2720	6220	2623803	2624048	246		
2721	6221	protein				

teosinte

2731	6231	2632543	2633100	558	prf:2324444A
		Mycobacterium avium pncA	48.1	74.6	185
		pyrazinamidase/nicotinamidase			
2732	6232	2633418	2633146	273	pir:E70870
		Mycobacterium ***tuberculosis***	42.7	80.0	75
		hypothetical protein			
		H37Rv Rv2520c			
2733	6233	2633600	2634064	465	sp:BCP_ECOLI
		Escherichia coli K12 bcp	46.8	73.8	141
		bacterioferritin. . . 6240	2649416	2648235	1182
		gp:SC4A7_14	Streptomyces coelicolor A3(2)	25.3	55.2
		404	hypothetical protein		
		SC4A7.14			
2741	6241	2649550	2650164	615	pir:D70716
		Mycobacterium ***tuberculosis***	40.4	60.9	230
		peptidase			
		H37Rv Rv0950c			
2742	6242	2650441	2650902	462	sp:Y077_MYCT
		Mycobacterium ***tuberculosis***	40.2	67.9	112
		hypothetical membrane protein			
		H37Rv Rv1343c			
2743	6243	2650986	2651339	354	sp:Y076_MYCLE
		Mycobacterium leprae	37.2	69.0	113
		hypothetical membrane protein			
		B1549_F2_59			
2744	6244	2652037	2651420	618	sp:Y03Q_MYCTU
		Mycobacterium ***tuberculosis***	55.0	76.7	202
		hypothetical protein			
		H37Rv Rv1341			
2745	6245	2652801	2652067	735	sp:RNPH_PSEAE
		Pseudomonas aeruginosa	60.2	81.4	236
		ribonuclease PH			
		ATCC. . . 15692 rph			
2746	6246	2653254	2653009	246	
2747	6247	2654018	2653326	693	
2748	6248	2654660	2654079	582	
2749	6249	2656236	2654875	1362	sp:Y029_MYCTU
		Mycobacterium ***tuberculosis***	29.0	58.2	428
		hypothetical membrane protein			
		H37Rv SC8A6.09c			
2750	6250	2656452	2656985	534	gp:AF121000_8
		Corynebacterium glutamicum	92.1	97.2	175
		transposase (IS1628)			
	492	gp:SCE22_22	Streptomyces coelicolor A3(2)		
	44.2	70.8 . 147	bacterial regulatory protein, marR		
		SCE22.22			
		family			
2756	6256	2661417	2660671	747	sp:Y03M_MYCTU
		Mycobacterium ***tuberculosis***	38.2	69.3	225
		hypothetical membrane protein			
		H37Rv Rv1337			
2757	6257	2661565	2662455	891	
2758	6258	2662376	2661417	960	pir:A47039
		Flavobacterium sp. nylC	30.2	58.3	321
		endo-type 6-aminohexanoate			
		oligomer hydrolase			
2759	6259	2662867	2662331	537	sp:Y03H_MYCTU
		Mycobacterium ***tuberculosis***	35.0	58.5	200
		hypothetical protein			

H37Rv Rv1332
2760 6260 2663182 2662883 300 sp:Y03G_MYCTU
Mycobacterium ***tuberculosis*** 57.1 77.1 105
hypothetical protein

H37Rv Rv1331
2761 6261 2663437 2664060 624
2762 6262 2664060 2665397 1338 sp:Y03F_MYCTU
Mycobacterium ***tuberculosis*** 61.2 80.8 428
hypothetical protein

H37Rv Rv1330c
2763 6263 2665687 2665992 306
2764 6264 2666115 2667854 1740 prf:1816252A
Escherichia coli dinG 25.2 53.3 647
ATP-dependent helicase

2765 6265 2668760 2667870 891 sp:Y0A8_MYCTU
Mycobacterium ***tuberculosis*** 29.7 60.1 313
hypothetical membrane protein

H37Rv Rv2560
2766 6266 2669561 2668839 723 pir:T34684
Streptomyces coelicolor A3(2) 39.0 52.0 222
hypothetical. . . sp:SERB_ECOLI Escherichia coli K12 serB
38.7 61.0 310 phosphoserine phosphatase

2768 6268 2671126 2672721 1596
2769 6269 2672805 2671063 1743 pir:D45335
Mycobacterium ***tuberculosis*** 46.8 74.4 575
cytochrome c oxidase chain I

H37Rv Rv3043c
2770 6270 2672950 2673255 306
2771 6271 2674339 2673338 1002 gp:AF112536_1
Corynebacterium. . . 6283 2683125 2682379 747
pir:S76790 Synechocystis sp. PCC6803 30.7 56.4
257 hypothetical protein

slr1563
2784 6284 2683418 2683131 288 pir:G70922
Mycobacterium ***tuberculosis*** 41.7 68.8 96
hypothetical protein

H37Rv Rv3129
2785 6285 2684646 2683627 1020 sp:ADH2_BACST
Bacillus stearothermophilus 26.1 52.8 337
alcohol dehydrogenase
DSM. . . 792

2789 6289 2690050 2688389 1662 sp:PGMU_ECOLI
Escherichia coli K12 pgm 61.7 80.6 556
phosphoglucomutase

2790 6290 2690150 2690437 288 pir:F70650
Mycobacterium ***tuberculosis*** 41.7 64.3 84
hypothetical membrane protein

H37Rv Rv3069
2791 6291 2690437 2690760 324 pir:D71843
Helicobacter pylori J99 jhp1146 25.4 61.5 122. . .
DET D . . . 2711308 672 prf:2509388L
Streptomyces collinus Tu 1892 28.1 54.1 196
oxidoreductase or dehydrogenase
ansG

2809 6309 2711850 2712374 525 sp:Y089_MYCTU
Mycobacterium ***tuberculosis*** 25.9 51.2 205
methyltransferase

H37Rv Rv0089
2810 6310 2713181 2713453 273 GSP:Y35814
Chlamydia pneumoniae 61.0 66.0 84
hypothetical protein

2811	6311	2713702	2718436	1254	sp:MURA_ACICA
	Acinetobacter calcoaceticus	44.8	75.3	417	
	UDP-N-acetylglucosamine 1-				
	NCIB 8250 murA				
	carboxyvinyltransferase				
2814	6314	2719750	2720319	570	sp:Y02Y_MYCTU
	Mycobacterium ***tuberculosis***		66.3	84.2	190
	hypothetical protein				
	H37Rv Rv1314c				
2815	6315	2721227	2720385	843	gp:SC2G5_15
	Streptomyces coelicolor A3(2)	45.9	69.0	281	
	transcriptional regulator				
	... brasilense ATCC	38.6	68.5	321	
	transcriptional regulator				
	29145 ntrC				
2828	6328	2732230	2731424	807	
2829	6329	2732636	2733367	732	pir:E70810
	Mycobacterium ***tuberculosis***		46.5	81.7	213
	phosphate transport system				
	H37Rv Rv0821c phoY-2				
	regulatory protein				
2830	6330	2734351	2733455	897	pir:S68595
	Pseudomonas aeruginosa pstB	58.8	82.8	255	
	phosphate-specific transport				
	component				
2831	6331	2735184	2734264	921	gp:MTPSTA1_1
	Mycobacterium ***tuberculosis***		51.4	82.2	292
	phosphate ABC transport system				
	H37Rv Rv0830 pstA1				
	permease protein				
2832	6332	2736215	2735202	1014	pir:A70584
	Mycobacterium ***tuberculosis***		50.2	78.5	325
	phosphate ABC transport system				
	H37Rv Rv0829 pstC2				
	permease protein				
2833	6333	2737538	2736414	1125	pir:H70583
	Mycobacterium ***tuberculosis***		40.0	56.0	369
	phosphate-binding protein S-3				
	H37Rv phoS2				
	precursor				
2834	6334	2738711	2737836	876	gp:SCD84_18
	Streptomyces coelicolor A3(2)	34.3	60.0	315	... 6336
	2740650 2739556	1095	sp:BMRU_BACSU		Bacillus
	subtilis 168 bmrU	24.7	55.2	344	
	hypothetical protein				
2837	6337	2740670	2741356	687	pir:E70809
	Mycobacterium ***tuberculosis***		44.9	74.2	225
	hypothetical protein				
	H37Rv Rv0813c				
2838	6338	2742577	2741636	942	gp:AF193846_1
	Solanum tuberosum BCAT2	28.6	56.0	259	
	branched-chain amino. ...	2742685	2743785	1101	
	gp:AB003158_6	Corynebacterium		58.5	79.0
	352	hypothetical protein			
	ammoniagenes ATCC 6872				
	ORF4				
2840	6340	2744010	2744222	213	pir:B70809
	Mycobacterium ***tuberculosis***		58.6	81.0	58
	hypothetical protein				
	H37Rv Rv0810c				

2841	6341	2745954	2744881	1074	gp:AB003158_5
	Corynebacterium		81.0	94.2	347
	5'-phosphoribosyl-5-aminoimidazole				
	ammoniagenes ATCC 6872	2747564	2746083	1482	
	gp:AB003158_4	Corynebacterium	70.3	89.0	
482	amidophosphoribosyl transferase				
	ammoniagenes ATCC 6872				
	purF				
2843	6343	2748057	2747683	375	pir:H70536
	Mycobacterium ***tuberculosis***		57.3	75.8	124
	hypothetical protein				
	H37Rv Rv0807				
2844	6344	2748095	2749111	1017	gp:AB003158_2
	Corynebacterium		75.9	94.0	315
	hypothetical protein				
	ammoniagenes ATCC	prf:2216389A			Aeromonas
	hydrophila JMP636	28.0	51.5	965	
	extracellular nuclease				
	nucH				
2854	6354	2756851	2757126	276	
2855	6355	2757815	2757129	687	pir:C70709
	Mycobacterium ***tuberculosis***		37.4	68.7	211
	hypothetical protein				
	H37Rv Rv0784				
2856	6356	2759200	2757863	1338	sp:DCTA_SALTY
	Salmonella typhimurium LT2	49.0	81.6	414	
	C4-dicarboxylate transporter				
...	6375	2780439	2780969	531	sp:YCDC_ECOLI
	Escherichia coli K12 ycdC	30.4	68.5	92	
	transcriptional regulator				
2876	6376	2780996	2782315	1320	pir:D70551
	Mycobacterium ***tuberculosis***		45.6	78.4	421
	hypothetical membrane protein				
	H37Rv Rv2508c				
2877	6377	2784481	2782340	2142	
2878	6378	2785615	2784656	960	gp:AF096929_2
	Rhodococcus erythropolis SQ1	2785651	705		
	sp.ALSR_BACSU	Bacillus subtilis 168 alsR	37.1	69.0	
	232	transcriptional regulator, LysR family			
2880	6380	2787782	2788594	813	pir:C70982
	Mycobacterium ***tuberculosis***		28.4	52.9	278
	hypothetical protein				
	H37Rv Rv3298c lpqC				
2881	6381	2789399	2788587	813	pir:C69862
	Bacillus subtilis 168 ykrA	26.7	55.6	288	
	2790152	2790550	399	pir:A45264	Oryctolagus
	cuniculus kidney	28.6	50.7	140	hypothetical
	protein				
	cortex rBAT				
2884	6384	2790946	2792448	1503	pir:B70798
	Mycobacterium ***tuberculosis***		36.0	64.0	464
	hypothetical membrane protein				
	H37Rv Rv3737				
2885	6385	2792531	2792857	327	pir:S41307
	Streptomyces griseus hrdB	32.3	50.3	155	
	transcription	6391	2797820	2798509	690
	gp:AF121672_2	Staphylococcus aureus 8325-4	31.4	63.2	
223	ABC transporter				
	mreA				
2892	6392	2798837	2799391	555	pir:E70507
	Mycobacterium ***tuberculosis***		60.0	87.4	135

hypothetical membrane protein
H37Rv Rv2060
2893 6393 2799535 2801034 1500 pir:A69426
Archaeoglobus fulgidus 23.4 52.5 303
transposase (ISA0963-5)
2894. . .
DETD . . . prf:2309303A Bradyrhizobium japonicum lrp
31.0 66.2 142 leucine-responsive regulatory
protein
2920 6420 2827817 2827458 360
2921 6421 2828383 2827904 480 pir:C70607
Mycobacterium ***tuberculosis*** 55.9 86.2 152
hypothetical protein
H37Rv Rv3581c
2922 6422 2829146 2828379 768 sp:Y18T_MYCTU
Mycobacterium ***tuberculosis*** 46.4 71.5 235
hypothetical protein
H37Rv Rv3582c
2923 6423 2829749 2829156 594 pir:H70803
Mycobacterium ***tuberculosis*** 73.3 91.1 157
transcription factor
H37Rv Rv3583c
2924 6424 2830057 2830779 723 prf:2214304A
Mycobacterium ***tuberculosis*** 43.5 70.0 223
two-component system response
H37Rv Rv3246c mtrA
regulator
2925 6425 2830779 2831894 1116 sp:BAES_ECOLI
Escherichia coli K12 baeS 29.3 . . 6428 2834188
2835285 1098 sp:YACK_BACSU Bacillus subtilis 168
yacK 40.3 73.3 345 hypothetical protein
2929 6429 2835969 2835283 687 pir:D70804
Mycobacterium ***tuberculosis*** 29.4 53.3 231
hypothetical protein
H37Rv Rv3587c
2930 6430 . 2837499 2836048 1452 gp:PPU96338_1
Pseudomonas putida NCIMB 59.5 85.1 471
p-hydroxybenzaldehyde
9866. . . L-2,3-butanediol dehydrogenase
2937 6437 2842130 2842453 324
2938 6438 2842493 2843233 741
2939 6439 2843405 2843716 312
2940 6440 2843722 2843432 291 pir:E70552
Mycobacterium ***tuberculosis*** 48.5 69.1 97
hypothetical protein
H37Rv Rv3592
2941 6441 2845139 2845558 420 GSP:Y29188
Pseudomonas aeruginosa 57.0 63.0 99
virulence factor
ORF24222
2942. . . 6452 2859055 2857613 1443 gp:AF237667_1
Corynebacterium glutamicum 100.0 100.0 481
lincomycin resistance protein
lmrB
2953 6453 2860145 2859195 951 pir:G70807
Mycobacterium ***tuberculosis*** 26.7 55.8 240
hypothetical protein
H37Rv Rv3517
2954 6454 2862082 2860505 1578 gp:AB012100_1
Bacillus stearothermophilus lysS 41.7 71.2 511

lysyl-tRNA synthetase
2955. . . 6465 2870444 2869863 582 gp:AF008931_1
Salmonella typhimurium GP660 51.5 83.0 165
hypoxanthine
hprt
phosphoribosyltransferase
2966 6466 2871389 2870499 891 sp:YZC5_MYCTU
Mycobacterium ***tuberculosis*** 41.0 66.8 310
cell cycle protein MesJ or cytosine
H37Rv Rv3625c
deaminase-related protein
2967 6467 2872677 2871445 1233 sp:DAC_ACTSP
Actinomyces sp. . . sp:IPYR_ECOLI Escherichia coli K12
ppa 49.7 73.6 159 inorganic
pyrophosphatase
2969 6469 2873611 2873393 219
2970 6470 2875443 2873905 1539 pir:H70886
Mycobacterium ***tuberculosis*** 56.0 80.7 507
spermidine synthase
H37Rv speE
2971 6471 2875832 2875434 399 sp:YOB1_MYCTU
Mycobacterium ***tuberculosis*** 38.6 86.4 132
hypothetical membrane protein
H37Rv Rv2600
2972 6472 2876280 2875870 411 sp:YOB2_MYCTU
Mycobacterium ***tuberculosis*** 36.8 63.2 144
hypothetical protein
H37Rv Rv2599
2973 6473 2876777 2876280 498 sp:YOB3_MYCTU
Mycobacterium ***tuberculosis*** 36.4 60.1 173
hypothetical protein
H37Rv Rv2598
2974 6474 2877385 2876777 609 sp:YOB4_MYCTU
Mycobacterium ***tuberculosis*** 44.6 72.3 202
hypothetical protein
H37Rv Rv2597
2975 6475 2877703 2877455 249 sp:PTBA_BACSU
Bacillus subtilis 168 bglP 30.3 59.6 89
PTS. . . dehydrogenase
2983 6483 2887833 2886916 918 gp:CJ11168X2_254
Campylobacter jejuni Cj0604 57.3 79.7 241
hypothetical protein
2984 6484 2890185 2890346 162 GP:MSGTCWPA_1
Mycobacterium ***tuberculosis*** 62.0 63.0 54
hypothetical protein
2985 6485 2890377 2890553 177 GP:MSGTCWPA_1
Mycobacterium ***tuberculosis*** 74.0 80.0 31
hypothetical protein
2986 6486 2890540 2888897 1644 gsp:R94368
Brevibacterium flavum MJ-233 99.5 100.0 548
heat shock protein or. . . MUC5B 21.7 42.3
1236 hypothetical protein
2994 6494 2906738 2903964 2775
2995 6495 2907250 2906639 612
2996 6496 2907515 2908885 1371 pir:G70870
Mycobacterium ***tuberculosis*** 37.1 68.0 447
peptidase
H37Rv Rv2522c
2997 6497 2909210 2909788 579
2998 6498 2909830 2909231 600
2999 6499 2910172 2913228 3057 prf:2504285B

Staphylococcus. . .
 DETD . . . 25.6 63.6
 121 Na⁺/H⁺ antiporter or multiple
 resistance and pH regulation related
 protein G
 3005 6505 2917617 2917024 594 pir:D70594
 Mycobacterium ***tuberculosis*** 24.7 54.5 178
 hypothetical protein
 H37Rv lipV
 3006 6506 2918757 2917630 1128 sp:YBDK_ECOLI
 Escherichia coli K12 ybdK 27.0 61.7 334
 hypothetical. . . 6508 2919715 2920293 579
 sp:DEF_BACSU Bacillus subtilis 168 def 37.5 60.9
 184 polypeptide deformylase
 3009 6509 2919741 2919490 252 pir:D70631
 Mycobacterium ***tuberculosis*** 47.9 70.4 71
 hypothetical protein
 H37Rv Rv0430
 3010 6510 2920286 2921290 1005 pir:B70631
 Mycobacterium ***tuberculosis*** 31.3 54.2 339
 acetyltransferase (GNAT) family or
 H37Rv Rv0428c
 N terminal acetylating enzyme
 3011 6511 2920476 2919808 669
 3012 6512 2920849 2920220. . . 936 sp:BCRA_BACLI
 Bacillus licheniformis ATCC 36.9 66.3 309
 ABC transporter ATP-binding protein
 9945A bcrA
 3022 6522 2929756 2929256 501 pir:C70629
 Mycobacterium ***tuberculosis*** 47.6 68.5 168
 mutator mutT protein
 H37Rv Rv0413
 3023 6523 2929951 2931336 1386 pir:B70629
 Mycobacterium ***tuberculosis*** 35.0 70.2 423
 hypothetical membrane protein
 H37Rv Rv0412c
 3024 6524 2931340 2932371 1032 sp:GLNH_BACST
 Bacillus stearothermophilus 31.5 64.8 270
 glutamine-binding protein precursor
 NUB36 glnH
 3025 6525 2932577 2934829 2253 pir:H70628
 Mycobacterium ***tuberculosis*** 41.2 63.5 805
 serine/threonine kinase
 H37Rv Rv0410c pknG
 3026 6526 2933398 2932652 747
 3027 6527 2938403 2939767 1365 sp:ADRO_BOVIN
 Bos taurus 37.2. . . 225
 3039 6539 2951723 2950434 1290 gp:AB003160_1
 Corynebacterium 89.7 95.3 427
 adenylosuccinate synthetase
 ammoniagenes purA
 3040 6540 2951933 2952691 759 pir:G70575
 Mycobacterium ***tuberculosis*** 34.3 59.3 204
 hypothetical protein
 H37Rv Rv0358
 3041 6541 2952709 2952972 264
 3042 6542 2954141 2952975 1167 sp:YFDA_CORGL
 Corynebacterium glutamicum 100.0 100.0. . . 2955523
 951 gp:CGFDA_1 Corynebacterium glutamicum

100.0	100.0	304	hypothetical protein		
AS019 ATCC 13059 ORF1					
3045	6545	2957447	2956830	618	pir:G70833
Mycobacterium		***tuberculosis***		76.9	91.2 182
methyltransferase					
H37Rv Rv0380c					
3046	6546	2958036	2957485	552	gp:AF058713_1
Pyrococcus abyssi		pyrE	39.1	65.5	174
orotate phosphoribosyltransferase					
3047	6547	2959110	2958139	972	pir:B70834
Mycobacterium		***tuberculosis***		27.6	60.0 250
hypothetical protein					
H37Rv Rv0383c					
3048	6548	2960371	2959520	852	sp:THTM_HUMAN
Homo sapiens		mpsT	29.6	56.1	294
3-mercaptopyruvate					
sulfurtransferase					
3049	2974382	183	gp:SCE20_34	Streptomyces	
coelicolor A3(2)		73.2	87.5 56	rifampin	
ADP-ribosyl transferase					
SCE20.34c arr					
3065	6565	2974467	2975591	1125	pir:E70812
Mycobacterium		***tuberculosis***		30.5	56.2 361
hypothetical protein					
H37Rv Rv0837c					
3066	6566	2975629	2976360	732	pir:D70812
Mycobacterium		***tuberculosis***		33.8	64.7 204
hypothetical protein					
H37Rv Rv0836c					
3067	6567	2976596	2977774	1179	pir:D70834
Mycobacterium		***tuberculosis***		31.9	60.6 386
oxidoreductase					
H37Rv Rv0385					
3068	6568	2978644	2977847	798	pir:B69109
Methanobacterium			32.0	67.3	275
N-carbamoyl-D-amino acid					
thermoautotrophicum Delta H.			2982023	438	
gp:SAU43299_2		Streptomyces albus G hspR		47.4	70.4
135 heat shock transcription regulator					
3074	6574	2983679	2982495	1185	sp:DNAJ_MYCTU
Mycobacterium		***tuberculosis***		56.7	80.1 397
heat shock protein dnaJ					
H37Rv RV0352 dnaJ					
3075	6575	2984522	2983887	636	sp:GRPE_STRCO
Streptomyces coelicolor		grpE	38.7	66.5	
DET D . . . gp:MLCB1883_3 Mycobacterium leprae					
31.2	54.8	529	hypothetical membrane protein		
MLCB1883.04c					
3154	6654	3050522	3051190	669	
3155	6655	3050592	3049456	1137	pir:G70961
Mycobacterium		***tuberculosis***		53.4	79.1 369
hexosyltransferase					
H37Rv Rv0225					
3156	6656	3051194	3051964	771	pir:F70961
Mycobacterium		***tuberculosis***		58.6	73.3 251
methyl transferase					
H37Rv Rv0224c					
3157	6657	3053891	3052062	1830	sp:PPCK_NEOFR
Neocallimastix frontalis		pepck	54.7	78.5	601
phosphoenolpyruvate. . .		6659	3055867	3056631	765

	sp:YGGH_ECOLI	Escherichia coli K12 yggH	35.7	67.2
241	hypothetical protein			
3160	6660	3056613 3057317	705	pir:E70959
	Mycobacterium ***tuberculosis***		69.1	85.0 207
	hypothetical protein			
	H37Rv Rv0207c			
3161	6661	3057328 3059643	2316	pir:C70839
	Mycobacterium ***tuberculosis***		42.3	72.3 768
	membrane transport protein			
	H37Rv Rv0206c mmpL3			
3162	6662	3059517 3058096	1422	
3163	6663	3059651 3060733	1083	pir:A70839
	Mycobacterium ***tuberculosis***		29.1	62.9 364
	hypothetical membrane protein			
	H37Rv Rv0204c			
3164	6664	3060733 3061095	363	pir:H70633
	Mycobacterium ***tuberculosis***		34.3	69.4 108
	hypothetical membrane protein			
	H37Rv Rv0401			
3165	6665	3062927 3061380	1548	gp:AF113605_1
	Streptomyces coelicolor A3(2)	49.7	76.9	523
	propionyl-CoA . . . synthase			
3167	6667	3069930 3068143	1788	prf:2310345A
	Mycobacterium bovis BCG	33.5	62.3	592
	acyl-CoA synthase			
3168	6668	3071140 3070214	927	pir:F70887
	Mycobacterium ***tuberculosis***		39.8	67.4 319
	hypothetical protein			
	H37Rv Rv3802c			
3169	6669	3071644 3071147	498	
3170	6670	3073620 3071650	1971	sp:CSP1_CORGL
	Corynebacterium glutamicum	98.6	99.5	(Brevibacterium
	flavum) ATCC			precursor
	17965 cop1			
3171	6671	3074047 3075447	1401	
3172	6672	3074075 3073857	219	
3173	6673	3076562 3075540	1023	sp:A85C_MYCTU
	Mycobacterium ***tuberculosis***		36.3	62.5 331
	antigen 85-C			
	ERDMANN RV0129C fbpC			
3174	6674	3078772 3076715	2058	pir:A70888
	Mycobacterium ***tuberculosis***		37.5	61.2 667
	hypothetical membrane protein			
	H37Rv Rv3805c			
3175	6675	3079848 3078853	996	sp:NOEC_AZOCA
	Azorhizobium caulinodans	27.1	51.5	295
	nodulation protein			
	ORS571 noeC			
3176	6676	3080351 3079848	504	pir:C70888
	Mycobacterium ***tuberculosis***		51.2	75.0 168
	hypothetical protein			
	H37Rv Rv3807c			
3177	6677	3082311 3080344	1968	pir:D70888
	Mycobacterium ***tuberculosis***		55.6	74.7 656
	hypothetical protein			
	H37Rv Rv3808c			
3178	6678	3082467 3083960	1494	
3179	6679	3084411 3083935	477	sp:BCRC_BACLI
	Bacillus licheniformis ATCC	28.2	6684	3088303
	3087101	1203	sp:GLF_ECOLI	Escherichia coli K12
	glf	43.2	72.9	377
	UDP-galactopyranose			

mutase						
3185	6685	3088616	3090664	2049	pir:G70520	
	Mycobacterium	***tuberculosis***		29.6	47.8	659
hypothetical protein						
	H37Rv	Rv3811	csp			
3186	6686	3092286	3090760	1527	sp:GLPK_PSEAE	
	Pseudomonas	aeruginosa		51.7	78.8	499
glycerol kinase						
	ATCC	15692	glpK			
3187	6687	3093175	3092342	834	pir:A70521	
	Mycobacterium	***tuberculosis***		41.6	70.3	279
hypothetical protein						
	H37Rv	Rv3813c				
3188	6688	3094050	3093175	876	pir:D70521	
	Mycobacterium	***tuberculosis***		46.7	72.0	261
acyltransferase						
	H37Rv	Rv3816c				
3189	6689	3095343	3094078	1266	gsp:W26465	
	Mycobacterium	***tuberculosis***		70.2	87.6	419
seryl-tRNA synthetase						
	H37Rv					
3190	6690	3095574	3096287	714	sp:FARR_ECOLI	
	Escherichia coli	K12 farR		27.7	61.7	235
transcriptional regulator, GntR family						
or fatty acyl-responsive regulator						
3191	6691	3096311	3097423	1113	pir:H70652	
	Mycobacterium	***tuberculosis***		32.6	61.2	356
hypothetical protein						
	H37Rv	Rv3835				
3192	6692	3097423	3097764	342	pir:A70653	
	Mycobacterium	***tuberculosis***		46.0	79.7	113
hypothetical protein						
	H37Rv	Rv3836				
3193	6693	3097878	3097780	99		
3194	6694	3098572	3097904	669	gp:AMU73808_1	
	Amycolatopsis	methanolica	pgm	37.2	...	pyk
3210	6710	3113390	3112449	942	gsp:Y25997	
	Brevibacterium	flavum	lctA	99.7	99.7	314
L-lactate dehydrogenase						
3211	6711	3113619	3115394	1776	pir:C70893	
	Mycobacterium	***tuberculosis***		33.5	64.8	526
hypothetical protein						
	H37Rv	Rv1069c				
3212	6712	3115407	3116042	636	gp:SC1C2_30	
	Streptomyces	coelicolor	A3(2)	32.1	58.5	224
hydrolase or. . . coli K12 MG1655						
				27.6	57.0	221
transcription activator or						
	glcC					
transcriptional regulator GntR family						
3215	6715	3117336	3118121	786	pir:B70885	
	Mycobacterium	***tuberculosis***		47.8	68.6	255
phosphoesterase						
	H37Rv	Rv2795c				
3216	6716	3118284	3119582	1299	sp:SHIA_ECOLI	
	Escherichia coli	K12 shiA		37.9	74.4	422
shikimate transport. . .						
DETD . . . transporter						
tetA						
3230	6730	3129785	3131395	1611		
3231	6731	3132920	3133030	111		

3232	6732	3133028	3131508	1521	
3233	6733	3133115	3133747	633	pir:G70654
		Mycobacterium ***tuberculosis***		33.8	64.8 216
		hypothetical protein			
		H37Rv Rv3850			
3234	6734	3135268	3133778	1491	prf:2508244AB
		Streptomyces cyanogenus lanJ	27.3	59.3	447
		membrane transport. . .	3139651	3140952	1302
		sp:SP3J_BACSU	Bacillus subtilis spoIIJ	26.0	53.6
		265	stage III sporulation protein		
3243	6743	3141523	3140885	639	pir:C70948
		Mycobacterium ***tuberculosis***		32.3	60.9 192
		transcriptional repressor			
		H37Rv Rv3173c			
3244	6744	3141969	3141709	261	sp:TAG1_ECOLI
		Escherichia coli K12 MG1655	34.5	71.3	87
		transglycosylase-associated protein			
		tagI			
3245	6745	3143356	3142454	903	sp:YW12_MYCTU
		Mycobacterium ***tuberculosis***		41.2	69.6 296
		hypothetical protein			
		H37Rv Rv2005c			
3246	6746	3144482	3143496	987	sp:YHBW_ECOLI
		Escherichia coli K12 MG1655	38.5	73.9	314
		hypothetical. . . activator			
3252	6752	3152413	3153828	1416	gp:SC4G6_31
		Streptomyces coelicolor	26.0	48.2	488
		hypothetical protein			
		SC4G6.31c			
3253	6753	3154766	3153894	873	sp:35KD_MYCTU
		Mycobacterium ***tuberculosis***		48.3	78.7 267
		hypothetical protein			
		H37Rv Rv2744c			
3254	6754	3154817	3154969	153	
3255	6755	3156697	3155246	1452	
3256	6756	3157373	3156306	1068	
3257	6757	. . . 882			
3306	6806	3189201	3187042	2160	sp:PBPA_BACSU
		Bacillus subtilis ponA	29.1	60.1	647
		penicillin-binding protein			
3307	6807	3189652	3189296	357	sp:Y0HC_MYCTU
		Mycobacterium ***tuberculosis***		41.1	72.0 107
		hypothetical protein			
		H37Rv Rv0049			
3308	6808	3189877	3190347	471	pir:B70912
		Mycobacterium ***tuberculosis***		35.1	65.0 137
		bacterial regulatory protein, marR			
		H37Rv Rv0042c			
		family			
3309	6809	3190378	3191319	942	sp:Y0FF_MYCTU
		Mycobacterium ***tuberculosis***		29.7	61.8 296
		hypothetical protein			
		H37Rv Rv2319c yofF			
3310	6810	3191354	3191848	495	
3311	6811	3192242	3191922	321	sp:YHGC_BACSU
		Bacillus subtilis yhgC. . . ybjZ			
3315	6815	3197186	3195210	1977	pir:E81408
		Campylobacter jejuni Cj0606	18.0	42.0	237
		hypothetical protein			
3316	6816	3197412	3198500	1089	pir:F70912
		Mycobacterium ***tuberculosis***		77.8	90.0 360

hypothetical protein
H37Rv Rv0046c

3317	6817	3199187	3198582	606	
3318	6818	3200686	3199202	1485	
3319	6819	3201754	3201260	495	sp:DPS_ECOLI. . .

zinc-binding dehydrogenase or

quinone oxidoreductase

(NADPH:quinone reductase) or

alginate lyase

3326	6826	3206646	3206756	111	
3327	6827	3206849	3208024	1176	sp:YDEA_ECOLI

Mycobacterium ***tuberculosis*** 26.4 66.3 398

membrane transport protein
H37Rv Rv0191 ydeA

3328	6828	3208279	3209454	1176	gp:AF234535_1
------	------	---------	---------	------	---------------

Corynebacterium melassecola 99.7 99.5 392

malate. . .

DET D . . . 3252728 3253480 753 sp:BU DC_KLETE

Klebsiella terrigena budC 26.9 52.9 238

acetoin(diacetyl) reductase (acetoin

dehydrogenase)

3376	6876	3253560	3253739	180	sp:YY34_MYCTU
------	------	---------	---------	-----	---------------

Mycobacterium ***tuberculosis*** 53.5 84.5 58

hypothetical protein
H37Rv Rv2094c

3377	6877	3255182	3253824	1359	sp:DTPT_LACLA
------	------	---------	---------	------	---------------

Lactococcus lactis subsp. lactis 34.5 71.6 469

di-/tripeptide. . . 6910 3291942 3290623 1320

sp:CCA_ECOLI Escherichia coli K12 cca 26.8 51.8

471 tRNA nucleotidyltransferase

3411	6911	3292532	3293497	966	pir:E70600
------	------	---------	---------	-----	------------

Mycobacterium ***tuberculosis*** 43.6 69.2 234

mutator mutT protein
H37Rv Rv3908

3412	6912	3292882	3292610	273	
3413	6913	3293497	3296007	2511	pir:F70600

Mycobacterium ***tuberculosis*** 25.8 54.3 858

hypothetical membrane protein
H37Rv Rv3909

3414	6914	3296156	3299404	3249	pir:G70600
------	------	---------	---------	------	------------

Mycobacterium ***tuberculosis*** 35.7 60.1 1201

hypothetical membrane protein
H37Rv Rv3910

3415	6915	3297706	3298428	723	
3416	6916	3299661	3300263	603	sp:RPSH_PSEAE

Pseudomonas aeruginosa. . . cwIB 51.0 75.4 196

N-acetylmuramoyl-L-alanine

amidase

3421	6921	3302765	3301989	777	
3422	6922	3303435	3304475	1041	
3423	6923	3303616	3302999	618	pir:D70851

Mycobacterium ***tuberculosis*** 34.4 58.5 212

hypothetical protein
H37Rv Rv3916c

3424	6924	3304787	3303636	1152	sp:YGI2_PSEPU
------	------	---------	---------	------	---------------

Pseudomonas putida ygi2 37.6 60.5 367

hypothetical protein
 3425 6925 3305671 3304835 837 sp:YG11_PSEPU
 Mycobacterium ***tuberculosis*** 65.0 78.0 272
 partitioning or sporulation protein
 H37Rv parB
 3426 6926 3306532 3305864 669 sp:GIDB_ECOLI
 Escherichia coli K12 gidB 36.0 64.7 153
 glucose inhibited division protein B
 3427 6927 3307632 3306682 951 pir:A70852
 Mycobacterium ***tuberculosis*** 44.7 75.4 313
 hypothetical membrane protein
 H37Rv Rv3921c
 3428 6928 3308369 3307971 399 sp:RNPA_BACSU
 Bacillus subtilis rnpA 26.8 59.4 123
 ribonuclease. . .

L6 ANSWER 3 OF 8 USPATFULL on STN

AN 2002:314401 USPATFULL

TI Molecular differences between species of the M. ***tuberculosis***
 complex

IN Behr, Marcel, Montreal, CANADA

Small, Peter, Stanford, CA, UNITED STATES

Schoolnik, Gary, Stanford, CA, UNITED STATES

Wilson, Michael A., Santa Clara, CA, UNITED STATES

PI US 2002176873 A1 20021128

AI US 2001-894844 A1 20010627 (9)

RLI Continuation of Ser. No. US 1999-318191, filed on 25 May 1999, PATENTED

PRAI US 1998-97936P 19980825 (60)

DT Utility

FS APPLICATION

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 Middlefield Road, Menlo Park, CA, 94025

CLMN Number of Claims: 23

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 3789

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Specific genetic deletion are identified in mycobacteria isolates,
 including variations in the M. ***tuberculosis*** genome sequence
 between isolates, and numerous deletion present in BCG as compared to M.
 tb. These deletions are used as markers to distinguish between
 pathogenic and avirulent strains, and as a marker for particular M. tb
 isolates. Deletions specific to vaccine strains of BCG are useful in
 determining whether a positive tuberculin skin test is indicative of
 actual ***tuberculosis*** infection. The deleted sequences may be
 re-introduced into BCG to improve the efficacy of vaccination.
 Alternatively, the genetic sequence that corresponds to the deletion(s)
 are deleted from M. bovis or M. ***tuberculosis*** to attenuate the
 pathogenic bacteria.

TI Molecular differences between species of the M. ***tuberculosis***
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AB Specific genetic deletion are identified in mycobacteria isolates,
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 BCG are useful in determining whether a positive tuberculin skin test is
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 sequences may be re-introduced into BCG to improve the efficacy of
 vaccination. Alternatively, the genetic sequence that corresponds to the
 deletion(s) are deleted from M. bovis or M. ***tuberculosis*** to
 attenuate the pathogenic bacteria.

SUMM [0001] ***Tuberculosis*** is an ancient human scourge that continues to be an important public health problem worldwide. It is an ongoing epidemic of staggering proportions. Approximately one in every three people in the world is infected with Mycobacterium ***tuberculosis***, and has a 10% lifetime risk of progressing from infection to clinical disease. Although ***tuberculosis*** can be treated, an estimated 2.9 million people died from the disease last year.

SUMM [0002] There are significant problems with a reliance on drug treatment to control active M. ***tuberculosis*** infections. Most of the regions having high infection rates are less developed countries, which suffer from a lack of easily accessible health services, diagnostic facilities and suitable antibiotics against M. ***tuberculosis***. Even where these are available, patient compliance is often poor because of the lengthy regimen required for complete treatment, and. . .

SUMM [0003] Prevention of infection would circumvent the problems of treatment, and so vaccination against ***tuberculosis*** is widely performed in endemic regions. Around 100 million people a year are vaccinated with live bacillus Calmette-Guerin (BCG) vaccine.. . . Unfortunately, the vaccine is widely variable in its efficacy, providing anywhere from 0 to 80% protection against infection with M. ***tuberculosis***.

SUMM [0004] BCG has an interesting history. It is an attenuated strain of M. bovis, a very close relative of M. ***tuberculosis***. The M. bovis strain that became BCG was isolated from a cow in the late 1800's by a bacteriologist named. . .

SUMM . . . as health care professionals likely to be exposed to tubercle bacilli. Recombinant DNA vaccines bearing protective genes from virulent M. ***tuberculosis*** are being developed using shuttle plasmids to transfer genetic material from one mycobacterial species to another, for example see U.S. Pat. No. 5,776,465. ***Tuberculosis*** vaccine development should be given a high priority in current medical research goals.

SUMM . . . BCG and virulent M. bovis. Subtractive genomic hybridization was used to identify genetic differences between virulent M. bovis and M. ***tuberculosis*** and avirulent BCG. U.S. Pat. No. 5,700,683 is directed to these genetic differences.

SUMM [0008] Cole et al. (1998) Nature 393:537-544 have described the complete genome of M. ***tuberculosis***. To obtain the contiguous genome sequence, a combined approach was used that involved the systematic sequence analysis of selected large-insert. . .

SUMM [0009] Mycobacterium ***tuberculosis*** (M. tb.) genomic sequence is available at several internet sites.

SUMM [0010] Genetic markers are provided that distinguish between strains of the Mycobacterium ***tuberculosis*** complex, particularly between avirulent and virulent strains. Strains of interest include M. bovis, M. bovis BCG strains, M. ***tuberculosis*** (M. tb.) isolates, and bacteriophages that infect mycobacteria. The genetic markers are used for assays, e.g. immunoassays, that distinguish between. . .

DETD . . . that serve as markers to distinguish between avirulent and virulent mycobacteria strains, including M. bovis, M. bovis BCG strains, M. ***tuberculosis*** (M. tb.) isolates, and bacteriophages that infect mycobacteria. These deletions are used as genetic markers to distinguish between the different. . .

DETD Identification of M. ***Tuberculosis*** Complex Deletion Markers

DETD . . . Rv2346c MTCY98.15c "H37Rv, segment 103: 17622, 26584"

SEQ ID NO:55 RD07 Rv2347c MTCY98.16c "H37Rv, segment 103: 17622, 26584"

SEQ ID NO:56 RD07 ***Rv2348c*** MTCY98.17c "H37Rv, segment 103: 17622, 26584"

SEQ ID NO:57 RD07 Rv2349c MTCY98.18c "H37Rv, segment

103: 17622, 26584"

SEQ ID NO:58 RD07 Rv2350c. . .

DETD . . . Collection, Rockville, Md, USA; SSI = Statens Serum Institute, Copenhagen, Denmark; CL = Connaught Laboratories, Willowdale, Canada, JATA = Japanese Anti- ***Tuberculosis*** Association; INH = isoniazid. Canadian BCG's refers to BCG-Montreal and BCG-Toronto, the latter being derived from the former.

DETD . . . of the fluorochrome tagged nucleotides used to label the selected probe. The strains used were the reference strain of Mycobacterium ***tuberculosis*** (H37Rv), other M. tb. laboratory strains, such as H37Ra, the O strain, M. tb. clinical isolates, the reference strain of. . .

DETD [0022] As used herein, the term "deletion marker", or "marker" is used to refer to those sequences of M. ***tuberculosis*** complex genomes that are deleted in one or more of the strains or species, as indicated in Table 1. The bacteria of the M. ***tuberculosis*** complex include M. ***tuberculosis***, M. bovis, and BCG, inclusive of varied isolates and strains within each species. Nucleic acids of interest include all or. . .

DETD . . . genomic sequence. For example, the deletion found in M. bovis, at Rv0221, corresponds to the nucleotide sequence of the M. ***tuberculosis*** H37Rv genome, segment 12: 17432,19335. The junction comprises the regions upstream of position 17342, and downstream of 19335, e.g. a. . .

DETD . . . of the provided deletion markers. Arrays of interest may further comprise other genetic sequences, particularly other sequences of interest for ***tuberculosis*** screening. The oligonucleotide sequence on the array will usually be at least about 12 nt in length, may be the. . .

DETD . . . particular infection or isolate is pathogenic. The term mycobacteria may refer to any member of the family Mycobacteriaceae, including M. ***tuberculosis***, M. avium complex, M. kansasii, M. scrofulaceum, M. bovis and M. leprae.

DETD [0060] Mycobacterium, particularly those of the M. ***tuberculosis*** complex, are genetically engineered to contain specific deletions or insertions corresponding to the identified genetic markers. In particular, attenuated BCG. . . are modified to introduce deleted genes encoding sequences important in the establishment of effective immunity. Alternatively, M. bovis or M. ***tuberculosis*** are modified by homologous recombination to create specific deletions in sequences that determine virulence, i.e. the bacteria are attenuated through. . .

DETD . . . an alternative embodiment, one or more of the deletions provided in Table 1 are introduced into a strain of M. ***tuberculosis*** or M. bovis. Preferably such a strain is reduced in virulence, e.g. H37Ra, etc. Methods of homologous recombination in order. . .

DETD . . . assay, mammalian macrophages, preferably human macrophages, are infected. In a comparison of virulent, avirulent and attenuated strains of the M. ***tuberculosis*** complex, alveolar or peripheral blood monocytes are infected at a 1:1 ratio (Silver et al. (1998) Infect Immun 66(3):1190-1199; Paul. . .

DETD . . . tb. complex bacteria are able to infect a wide variety of animal hosts. One model of particular interest is cavitary ***tuberculosis*** produced in rabbits by aerosolized virulent tubercle bacilli (Converse et al. (1996) Infect Immun 64(11):4776-4787). In liquefied caseum, the tubercle. . . and also to other people. Of the commonly used laboratory animals, the rabbit is the only one in which cavitary ***tuberculosis*** can be readily produced.

DETD . . . known in the art. Vaccines of the modified bacteria are administered to a host which may be exposed to virulent

2

tuberculosis . In many countries where ***tuberculosis*** is endemic, vaccination may be performed at birth, with additional vaccinations as necessary. The compounds of the present invention are.

DETD [0081] Therefore, with the preparation for an array that contained the whole genome of Mycobacterium ***tuberculosis***, we compared BCG-Connaught to Mycobacterium ***tuberculosis***, using the array for competitive hybridization. The protocol follows:

DETD . . . different fluorescent dyes, it is possible to determine that a spot of DNA on the array has hybridized to Mycobacterium ***tuberculosis*** (green dye) and not to BCG (red dye), thus demonstrating a likely deletion from the BCG genome.

DETD . . . probing for different DNA sequences. For the purposes of this project, we include DNA from the reference strain of Mycobacterium ***tuberculosis*** (H37Rv), from other laboratory strains, such as H37Ra, the O strain, from clinical isolates, from the reference strain of Mycobacterium. . .

DETD . . . of the genome database is performed to determine whether the sequence is exactly identical to one part of the Mycobacterium ***tuberculosis*** genome, and that the next part of the amplicon is exactly identical to another part of the Mycobacterium ***tuberculosis*** genome. This permits precise identification of the site of deletion.

DETD [0097] emb[Z79701|MTCY277 Mycobacterium ***tuberculosis*** cosmid Y277

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 1

LENGTH: 1773

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 1

atgactgctg aaccggaagt acggacgctg cgcgaggttg tgctggacca gctcggcact 60
gtggaatcgc gtgcgtacaa gatgtggctg ccgcccgtga ccaatccggt cccgtcaac 120
gagctcatcg cccgtgatcg gcgacaaccc ctgcgatttg ccctggggat. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 2

LENGTH: 297

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 2

atggaaaaaa tgcacatga tccgatcgt gccgacattg gcacgcaagt gagcgacaac 60
gctctgcacg cgtgtacgcg cggctcgacg gcgctgacgt cggtagccgg gctggttccc 120
gcgggggccc atgaggtctc gcgccaagcg gcgacggcgt tcacatcgga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 3

LENGTH: 1104

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 3

atgctgtggc acgcaatgcc accggagcta aataccgcac ggctgatggc cggcgcggg 60
ccggtcccaa tgcctgcgcg gcccgcggga tggcagacgc ttctggcggc tctggacgct 120
caggccgtcg agttgaccgc gcgcctgaac tctctgggag aagcctggac. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 4

LENGTH: 300

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 4

atggcagaga tgaagaccga tgccgctacc ctgcgcagg aggcaggtaa ttctgagcgg 60
atctccggcg acctgaaaa ccagatcgac caggtggagt cgacggcagg ttcgttcgag 120
ggccagtggc gcggcgcggc ggggacggcc gccacggccg cgggtgtgcg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 5

LENGTH: 285

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 5

atgacagagc agcagtggaa ttctcggggt atcgaggccg cggcaagcgc aatccaggga 60
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtcctgac caagctcgca 120
gcggcctggg gcggtagcgg ttctggaggcg taccagggtg tccagcaaaa. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 6

LENGTH: 1998

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 6

atggcgccgc actacgacaa gctcttcggt ccgcacgaag gtatggaagc tccggacgat 60
atggcagcgc agccgttctt cgaccccagt gcttcgttc cgccggcgcc cgcacggca 120
aacctaccga agcccaacgg ccagactccg cccccgacgt ccgacgacct. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 7

LENGTH: 1533

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 7

ttgagcgac ctgctgttgc tgctgtcct accgccgagg gggcaaccgc tgcgcggcct 60
gccaccaccc ggggtgacgat cctgaccggc agacggatga ccgatttggg actgccagcg 120
gcggtgccga tggaaactta tattgacgac accgtcgagg tgctttccga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 8

LENGTH: 840

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 8

atggctgaac cggtggccgt cgatcccacc ggcttgagcg cagcgccgc gaaattggcc 60
ggcctcgttt ttccgcagcc tcggcgccg atcgcggtca gcggaacgga ttgggtgta 120
gcagcaatca acgagacct gccagcatc gaatcgctgg tcagtacgg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 9

LENGTH: 2187

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 9

atgagtatta ccaggccgac gggcagctat gccagacaga tgctggatcc gggcggtggt 60
gtggaagcgc atgaagacac ttctatgac cgggccagg aatatagcca ggtttgcaa 120
agggtcaccg atgtattgga cactgcccgc cagcagaaag gccacgtctt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 10

LENGTH: 426

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 10

atggccggac tgaacattta cgtgaggcgc tggcggacag cgttcacgc aaccgtgtcg 60
gcattgatag ttccatctct cggactcgcc atcacccgg tcgtagtgc ggcgacggcc 120
agggcgacgt tctcggtgac atcgactgg cagaccggtt tcacgcccg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 11

LENGTH: 597

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 11

gtgaactcac cactgtctcg cggttctcg gctgcttca cgctgatcgc cgcgattggc 60

gcgcagaacg cattcgtgct gcggcaggga atccagcgtg agcacgtgct gccggtggtg 120
gcgctgtgca cgggtgccga catcgtgctg atcggcccg gtagcgagg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 12

LENGTH: 909

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 12

atggtggatc cgcagcttga cggccacag ctggccgcat tggctgccgt ggtcgaactg 60
ggcagcttcg atcgggccgc ggagcgccta catgtaccc cgtcggtgt cagtacgcgc 120
atcaagtctg tggagcagca ggtcggccag gtgctgtgg tcaggaaaa. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 13

LENGTH: 651

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 13

atgactccac gcagcctgt tgcacgtt ggtgtcgtgg ttgcagcac ctggcgctg 60
gtgagcgac cgcggcgcg tctgcccgc catcggtat cgtgtcga catcgcggtc 120
gtttcgtc gcgcacgca tcaggcttct ggtctggcg acgtcggtga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 14

LENGTH: 1674

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 14

gtgtcattc tggctgtgt tcccgagttc ttgacgtcc gcgcagcgga tgtggagaac 60
ataggtcca cactgcgcgc ggcaatgcc gcgctgccg cctcgaccac cgcgttgcg 120
gccgtggcg ctgatgaggt atcgcgcgcg gtggcagcg tgtttccag. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 15

LENGTH: 1674

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 15

gtgtcattc tggctgtgt tcccgagttc ttgacgtcc gcgcagcgga tgtggagaac 60
ataggtcca cactgcgcgc ggcaatgcc gcgctgccg cctcgaccac cgcgttgcg 120
gccgtggcg ctgatgaggt atcgcgcgcg gtggcagcg tgtttccag. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 16

LENGTH: 417

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 16

atgatcgtg acacaagcgc cgtggtggcc ctggtcaag gcgagggcc gcacgccacc 60
ctggtcgcg cgcctggc cggcgcccat agccccgtca tctcgcacc caccgtgcc 120
gaatgcctga ttgtttgac cgcccgctac ggccccgtg cgcgcacgat. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 17

LENGTH: 684

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 17

gtgcgcatca agatctcat gctgtcacg gctgtgtt tctctgtt ttcgggtgtg 60
gccacggccg cgccaagac ctactgcgag gattgaaag gcaccgatac cggccaggcg 120
tgccagatc aaatgtcca cccgcctac aacatcaaca tcagcctgcc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 18

LENGTH: 684

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 18
gtgcgcatca agatctcat gctgtcacg gctgtcgtt tgctctgtt ttcgggtgtg 60
gccacggcgc cgcccaagac ctactgcgag gatttgaaag gcaccgatac cggccaggcg 120
tgccagattc aaatgtccga cccggcctac aacatcaaca tcagcctgcc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 19

LENGTH: 1443

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 19

gtggtcgccc cgcggacgag aggatatgcg atccacaagc tgggtttctg cagcgtcgtc 60
atgctcgga tcaactgat aatcgcgcc ggtatctcc taactccagg tgaggatgac 120
gggctgcgag gacccttcgc gccgatgcc tatgttttag ctggcattt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 20

LENGTH: 846

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 20

atgggtgagg cgaacatccg cgagcaggcg atgccacga tgccacgggg tggccccgac 60
gcgtcttggc tggatcgtcg attccagacc gacgactgg agtacctga ccgcgacgat 120
gtgcccgatg aggtcaaaca gaagatcatc ggggtgctcg accgggtggg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 21

LENGTH: 1407

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 21

gtgagataca ctacacctgt gcgtgtgtgt gtctacctcc gaatctcaga agaccgctcc 60
ggcgaaacgc tcggcgtggc ccgccaacgc gaggactgcc taaagctgtg cgggcagcga 120
aaatgggtgc ccgtcgagta cctcgacaac gacgtcagcg catcaaccgg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 22

LENGTH: 513

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 22

atgagccggc accacaacat cgtgatcgtc tgtgaccacg gccgcaaagg cgatggccgc 60
atcgaacacg agcgtcgca tctgtcgcg ccgatcattt ggtcgacga gaccagggc 120
tggttacgc aggcgccagc ggtggcaaca ttactcgacg acgacaacca. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 23

LENGTH: 219

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 23

gtgtcgacca tctaccatca tcgcggccgc gtagccgcac tgtctcgttc ccgcgcatcc 60
gacgateccg agttcatgc cgcgaaaacc gatctcgttg ccggaacat cgcggactac 120
ctcatccga cctcgcgcg agcgcgcgcc ctgactgacg agcagcgcac. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 24

LENGTH: 396

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 24

atgaccggcg gcgcccggcg gtcgcccgcg acgcgacgat gcccgccac ggaggaccgg 60
gcaccccgca cagtcgccac accgtctagc gccgatccta ccgctcacg cgccgtgtcg 120
tggtgtcgg tgcacgagca tgtcgcgcg gtcctggatg ctgccgggtc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 25

LENGTH: 1413

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 25

atggccgaca tcccctacgg caccgactat cccgacgccc cctggatcga ccgggacggg 60
cacgtgctca tcgacgacgg tggcaaaccg acgcaagttc atcgcggccca agcccgaatc 120
gcctaccggc tagccgaacg ttaccaggac aagctgctgc acgtggccgg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 26

LENGTH: 393

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 26

atgaccgctg tcgcatcac cccggcatcc ggcggtcggc acagcgtccg attcgctac 60
gactctcga tcgtgtggt gatcaagtc acgaccccg cctatgcccg ctctgtgtcc 120
gcgcacaccc gctgtggtt catcgacgt gactggacc cactgtggc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 27

LENGTH: 270

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 27

atggctgaaa cccccgacca cgccgaactg cggcgacgaa tcgccgacat ggctttcaac 60
gccgatgtcg gtatggcgac ctgcaaaccg tgtggtgac cgtgccgta catcatctg 120
ccgaacctgc agaccggcga acccgatcg ggtgtcgccg acaacaaatg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 28

LENGTH: 312

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 28

gtgacccga tcaaccggcc cctgaccaac gacgaacgac aactgatgca cgagctggca 60
gtccagggtg tctgtcgca gacgggttgc tcaccgatg cggcggtcga agcactcgaa 120
tccttcgca aagacggaac acttatctc cgcggcgaca ccgagaacgc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 29

LENGTH: 468

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 29

atgccaaagc caccgaaacc ggcccggctc aaactggtg agggccgctc ccccgccgc 60
gattccggcg gccggaagt ccccgagtcg ccgaagtta tccgtcaggc accgatgcc 120
ccgaactggc tcgacgccga ggcgctggcc gaatggcggc gcgtcgacc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 30

LENGTH: 510

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 30

atggccgagc tgcggtctgg cgaaggccga accgtgcacg gcaccatcgt gccctacaac 60
gaggcgacca ccgtccgca cttcgacggc gagtccagg aaatgttcgc tcttggcgct 120
tttcggcgct ccacgcgga gcgcggccac aaattgaagc tgctgtctc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 31

LENGTH: 1419

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 31

atgaccgaat tcgacgacat caaaaacctc tctttacct aaaccgtga cgcggcgaag 60
cagctcctcg acagtgtcgc cgcgacctg accggtgagg cggcgacgcg tttcaggcg 120
ctgacgcgcc acgccgagga actcgggcg gagcagcgcc gcccgggccg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 32
 LENGTH: 351
 TYPE: DNA
 ORGANISM: Mycobacteria ***tuberculosis***
 SEQUENCE: 32
 atggcgccgc tggccgccc atgccgagc tggaacggcc gaaagccaag cagcggaac 60
 aggaaggcgc cgaccatggc cgccaggctc gatattctgg ctggggccc atggcccca 120
 agccagaatc ggagcgtcgt tcgacgaaa cagacactgc tatcgcgca. . .
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 37
 LENGTH: 1461
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 37
 atgtctgaca gtgccaggga atacgacaag cttttcatcg gcggcaagtg gaccaaaccg 60
 tcgacctccg atgttatcga ggtacgtcgc ccagccactg gggaatatgt cggcaagggtg 120
 ccgatggcgg ccgccgccga cgtcgacgcc gcggtcgccg cagcacgtgc. . .
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 38
 LENGTH: 831
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 38
 atggcacgtc gcgatgtcct ggtctccgcc gactgggctg agagcaatct gcacgcgccg 60
 aaggtcgttt tcgtcgaaat ggacgaggac accagtgcac atgaccgtga ccatattgcc 120
 ggccgcatca agttggactg gcgcaccgac ctgcaggatc cggtaaacg. . .
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 39
 LENGTH: 300
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 39
 atgtctctg gaccaagca aggactgaca ttgccggcca gcctcgacct ggaaaaagaa 60
 acggtgatca ccggccgcgt agtggacggt gacggccagg ccgtggcgcg gcgcttcgtg 120
 cggctgctgg actctccga cgagttcacc gcggaggctg tcgctcgccg. . .
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 40
 LENGTH: 441
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 40
 atggccaatg tggtagctga aggtgcctac cttactgtc ggctcactga tcagccgctg 60
 agtgtggacg aagtgtctag ccgctctcg ggccccgaac aaggcggcat tgtcatatt 120
 gtgggaaacg tgcgtacca caatgccggg catgatgta cgcggttgtt. . .
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 41
 LENGTH: 600
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 41
 atgagtcctg ctccatcgcc cctgctcgcc gaccaccgg accgcattcg ttggaacgcg 60
 aaatacgagt gcgctgaccc cagcgaggcg gtattgcgc ccatatctg gctcggcgac 120
 gtgctgcagt tcggggtgcc agaaggccg gttctggaac tggcgtcgcg. . .
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 48
 LENGTH: 1020
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 48
 gtgaagegag cgctcatcac cggaatcacc ggccaggacg gctcgtatct cgccgaactg 60
 ctgctggcca aggggtatga ggttcacggg ctcatccggc gcgcttcgac gttcaacacc 120

tcgcgatcg atcacctcta cgtcgaccg caccaaccg gcgcgggct. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 49

LENGTH: 966

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 49

atgaacgcgc acacctcggc cggcccgtt gaccgcgcgg cccgggtcta catcgccggg 60

catcgccggc tggtcgggtc cgcgctgcta cgcacgttg cgggcgcggg gttcaccaac 120

ctgctgtgc ggtcacgcgc cgagcttgat ctgacggatc gggccgcgac. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 50

LENGTH: 729

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 50

atgaggctgg cccgtcgcgc tcggaacatc ttgcgtcgca acggcatcga ggtgtcgcgc 60

tactttgcc aactggactg ggaacgcaat ttcttgccc aactgcaatc gcatcgggtc 120

agtgccgtgc tcgatgtcgg ggccaattc gggcagtagc ccagggtct. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 57

LENGTH: 1524

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 57

atgtcacgcc gagcattct ggtaaggcg gctggagccg gggcagcggc ggtttgacg 60

gactgggccg caccggtgat cgaagggcc tatggtccg gtcctgtc ggtcatttg 120

accgatatcg agcacatcgt gctgtgccta caggagaaca ggtcgttca. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 58

LENGTH: 1536

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 58

atgtcacgc gagagtttt gacaaagctc actggcgag gcgcagcggc attcctgatg 60

gactgggctg caccggtgat tgaaaaggcc tacggcgccg ggcctgtcc cggacatttg 120

accgatatcg agcatatcgt gttgctgatg caggagaacc ggtcattca. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 59

LENGTH: 1536

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 59

atgtcacgc gagagtttt gacaaagctc actggcgag gcgcagcggc attcctgatg 60

gactgggctg caccggtgat tgaaaaggcc tacggcgccg ggcctgtcc cggacatttg 120

accgatatcg agcatatcgt gttgctgatg caggagaacc ggtcattca. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 66

LENGTH: 720

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 66

atgatccgat tggtcgcta ttgatgcc ctggtggccg ccggccttc cgcgcattg 60

tcggggtgcg attccacaa ctcgggatcg ctcggtgccg atccgcggca ggtgaccgtg 120

ttcggaaccg ggcaagtga ggggtgtccg gacacgtga tcgctgacgt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 72

LENGTH: 966

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 72

atggg'gcac ctaccgaacg gttagtgtat accaacggcg tgcgactgcg agtggtcgag 60
gccggtgagc ccggcgcacc cgtggtgata ctggcccacg gctttccga actggcctat 120
tcatggagac accagattcc tgcgcttgcc gacgccggt accacgtgt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 81

LENGTH: 1170

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 81

atgatcatcg ttgtcgggat cggcgcgcac ggcatgaccg gtctctccga gcattctgc 60
tccgaattgc gcagggccac agtaatttac ggctcgaaac ggcaacttgc cctgctcgac 120
gataccgtca ccgccgagcg ctgggagtgg ccgacgccga tgcgcccgc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 92

LENGTH: 624

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 92

ttgccatgc cagcaaccgc ccgaccggac accgccacgg tgggagagcg tgtgcgcgt 60
caagttttat ggggcgtttt ttggcatcat ggcatctcg acccgaaacc cggaaagagg 120
agggtgtgtg tgaatatggg taggcgtgtg ccgcgcgcgg cgccggcgca. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 93

LENGTH: 321

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 93

ttgaccaca agcgcactaa acgccagcca gccatgcgcg cagggtctaa cgccccgcgt 60
cggaatcgcg ttggcgcgca acatggttgg ccggccgacg ttccgtccgc cgagcagcgc 120
cgcgcccaac ggcaagcgca cctcgaggct atccgcgcgag cgtacgccga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 94

LENGTH: 243

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 94

atgagcgcc acgcgttggc tgctcggacg ttgctggccg ccgcggacga gcttgcggc 60
ggcccgccag tcgaggcttc ggccgcgcg ctggccggcg acgcccggg cgcatggcgg 120
accgcggccg tcgagcttgc gcgagcgtt gtccgcgctg tggcggagtc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 95

LENGTH: 1425

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 95

atggctgaca tcccctacgg ccgtgactat ccgaccgga tctggtgtga cgaggacggc 60
cagccgatgc cgccggtcgg cgccgaattg ctgcagaca ttagggcatt cttgcggcgg 120
ttcgtagtct atccaagcga ccatgaactg atcgcgcaca cctctggat. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 96

LENGTH: 390

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 96

atgaccgcc tcggcgggtc gccccgcacg cgacgatgcc cgccacaga ggaccgggca 60
cccgcacag tcgccacac gtctagacc gatctaccg cgtcccgcgc cgtgtcgtgg 120
tggtcggtc acgagtaigt cgcaccgacc ctggccgccg ccgtggaatg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 97

LENGTH: 258

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 97

atgtgcgcgt tcccgctgcc gagtctcggg tggacggtct ctcacgagac cgaaggcccc 60
ggcatggcag acgtcccc gttgtcacgg cggatcatca cgtacagtga ggccgccgaa 120
tatctagcgg tcaccgaccg cacggctcgc cagatgatcg ccgacggccg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 98

LENGTH: 360

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 98

atggccgatg cggttaagta cgtagttagt tgcaactgcg acgacgaacc gggagcgctc 60
atcatcgctt ggatcgacga cgaacgaccc gccggcgggc acatacatag cgggtcgaa 120
accgcttca ccgaaacaca gtggggccgc catatcgagt ggaaactga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 99

LENGTH: 1125

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 99

gtgacgcaaa ccgcaagcg tcagagacgc aaattcggtc gcatccgaca gttcaactcc 60
ggccgctggc aagccagcta caccggcccc gacggccgcg tgtatcgcg ccccaaaacc 120
ttcaacgcca agatcgacgc cgaagcatgg ctaccgacc gcccccgga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 100

LENGTH: 225

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 100

gtgatagcgg gcgtcgacca ggcgcttgca gcaacaggcc aggctagcca gcggcgcgca 60
ggcgcatctg gtggggtcac cgtcgtgtgc ggcgtgggca cgaacagag gaacctttcg 120
gtggttcac cgagtcagtt cacatttagt tcacgcagcc cagattttgt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 101

LENGTH: 186

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 101

atgatcgagc agggcccgca ctgccgggac gtggtcaccc agctcgccgc ggtatcgcg 60
gcactcgacc gcgcgggatt caagatcgtt gcgcgagggt tgaaggatg cgtgtccggg 120
gccacggcca gcggcgcggc accgctgagt gcagctgagc tagaaaaagt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 102

LENGTH: 357

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 102

atgtcggacc agccacgta tcaccaggtc ctgacgacc tgetgcccc acaccgcgct 60
ctacgtcacc agattccca ggtgtaccag cgattttag ccctgggcga cgcccgctt 120
accgacggcg ctctcagccg caaggtaag gagcttggg cgctggcgat. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 103

LENGTH: 1854

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 103

atgtcctatc tcgtcgtggt gccggagttg gtcgcagcgg cggcaacaga ttggcgaac 60
atcgtttcgt cgattagtgc agccaacgcg gccgcggcgg caccgaccac ggcaactgtc 120
gcagccggcg gcgacgaggt atcggcggcc atagccgctg tttcggagc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 104

LENGTH: 1242

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 104

gtgcatgagg tggctgctg tgagcaacgt tcggacgggc cgatgaggct ggatgcgcag 60
ggccgactgc agcgttacga ggaggcggtc gctgactacg atgcaccgtt tgcgttcgta 120
gatctcgacg cgatgtgggg caatgccgat caactgcttg cgcgcgccgg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 105

LENGTH: 1284

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 105

atggacgagg cccaccggc tcaccggca gatcggggc ggcccgggtg cccaattcaa 60
ggcgcgcgaa gaggagctgc catgacaccg atcaccgcc tgcgaccga gttggcggcc 120
atgcgcgagg tagtcgagac gctcgaccc attgagcgtg ccgcggcgca. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 106

LENGTH: 1284

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 106

atgagcccga tatggagtaa ttggcctggt gagcaagtct gcgcgccgtc ggcgatcgta 60
cggccgacct cggaggctga gctggccgac gtgatcgcg aggcggcgaa aagaggcgag 120
cgggtacgcg cggttggcag cgggcattcg ttaccgaca tcgctgcac. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 107

LENGTH: 309

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 107

ttgggtcaa caggaggtag ccaaccatg acggcgaatc gagggcccgc tgcaatctcg 60
agcggtcga actctggccg cgttctcgac accgccggg gtatctcat cgctcttcgg 120
cggtgccccg cagagaccgc gttcgacgag ttgcacaacg ccgctcaacg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 108

LENGTH: 744

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 108

gtgccacctc cggaaggaaa gtcgacaacg aatcgcgacg aaggcatcca ggtgctccgt 60
cgcgccgtcg ccgcgttgga cgaaatagct gccgaaccgg gacacctgcg cctagtcgat 120
ctctcgagc ggctggggct ggccaaatcg acgactcgac gcttgctggt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 109

LENGTH: 1218

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 109

atggcatcgg tcgcccaacc cgtaggcgc cgcccaaagg accggaagaa gcagatttg 60
gatcaggccg ttgactgtt catgaaactg gcttccatt cggtaaat ggaggacatt 120
gccgaggcgg ccggggtgac cgcgcgcgcg ttgatcgcc actacgacaa. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 110

LENGTH: 795

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 110

atggaatcg tggccgacaa ggcgccggt cgggtcgtg atccggtctt gcggccggtg 60
ggcgcgctgg gcgatttct cgcgatgacg ctgcacactg ccgtgtgcat gttcaagccg 120
cctttcgct ggctgaata cctactcag tctgtgtcg tggcgcggt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 111

LENGTH: 813

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 111

atgacggcag cgaagccct tgtaagcgaa tggaatcgga tgggatcgca gatgcggttc 60
ttcgtcggca cgtggccgg gattcccgac gccctcatgc actaccgagg cgagctgctg 120
cgggtgatcg cgcaaatggg gttggggacc ggggttcttg cggtgatcgg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 112

LENGTH: 1275

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 112

atgagacgag ggcgggctg acaccgtttg cagcagcgt ggtggacgct gatcctgttc 60
gcggtgatcg ggtggctgt cctggtgacg gcggtgtcct tcacgggag cttgcggctg 120
actgtcccg tgacgtggc ggccgaccgc tccgggctgg tgatggactc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 113

LENGTH: 1026

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 113

atgagggaga acctggggg cgtcgtggtg cgcctcggcg tcttctggc ggtatgcctg 60
ctgacggcgt tctgtctgat tgccgttctc ggggaggtgc gcttcggcga cggcaagacc 120
tactacggcg agttcgcaa cgtgtccaat ctgcaacgg gcaagctggt. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 114

LENGTH: 1230

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 114

atgaaatcct tcgccgaacg caaccgtctg gccatcgga cagtcggcat cgtcgtcgtc 60
gccgccgttg cgtggccgc gctgcaatac caggggctgc cgttttcaa ccagggcacc 120
agggttcgg cctatttcg cgacccggc gggctcgca ccggcaacac. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 115

LENGTH: 1269

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 115

gtgacaaga aactcagacg tgcccgtcg gtgttgcgga ccgccctggt gctgctcggc 60
ggcgtgatcc tggccatcg caccgccgac gccgccgcc gcacgaccgt ggtgcctac 120
ttcgacaaca gcaacgtgt gtgcgccgt gacgacgtgc tcattcgggg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 116

LENGTH: 1131

TYPE: DNA

ORGANISM: M. ***tuberculosis***

SEQUENCE: 116

gtgaggatcg gctgaccct ggtgatgat gcggccgtgg tagcgagctg cggctggcgc 60
gggtgaatt cgtgccgtg gcccgacg cagggcaacg gccggggtc cttcgggtc 120
caggcgagc tgccgatgt caacaacac cagccgaact cgcgggtgcg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 117

LENGTH: 1311

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 117

atgctgcatc taccgccc agtgatggt cagctggccg tctttaccgt gatcgggtg 60

ggcgtgctgg ccatcacgtt cctgcatttc gtgaggctgc cggcgatgct ttccggcgtc 120
ggccgctaca cggtagacat ggagctggtc gaagccggtg ggctgtatcg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 118

LENGTH: 573

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 118

atgtcggtag cagtggattc cgaccccgag gatgacgccg tatcgagat cgctgaggca 60
gccggcgtgt cgccggcccc agccaaacca tccatgtcgg cgccgcggcg catgtgctg 120
ttcggcctgg tcgtcgtcgt cgctttggcg gtgctgtgt gttgctgggg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 119

LENGTH: 480

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 119

gtgagctggt cgccgggtgat cgccacggg ctgctgcccg ggctggcggt ggccgtgacg 60
tgtggcgccg gcttgtgtaa atggcaggac ggccgctcc gcgacgccgc ggttgccgt 120
gcggaatccg tgcggggccg gaccgacggc accaccgcgc tgctgtctta. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 120

LENGTH: 375

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 120

gtgcagcgcc aatcattgat gcccagcag acccttgccg ccggcggttt cgtgggtgcg 60
ctgctatgcg gtgtcgtgac ggccgcggtg ccaccacag caccgcccga cgtggtcgcc 120
tatctgttca acgtgacgtt acgcccgggc tacaactcg ccaacgccga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 121

LENGTH: 663

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 121

atgtcgcgtc gacatcggc cactgtgcc ttgtccgga ccaccgccgt cgccataatg 60
gtgtctccc cgccacgggc cgacgacaag cggtcaacg acggcgtggt cgccaacgtc 120
tacaccgttc aacgtcaggc cggtgcacc aacgacgtca cgtcaaccc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 122

LENGTH: 405

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 122

gtcgggtgga ttgtcgacgg tatgaacgtg atcgaagtc gtccggatgg ttgtggcgcc 60
gaccgccatc gcgcgatggt gatgctggtg gaaaggctcg aggggtgggc catcaccaag 120
gtcggggcgc acgacgtgac ggtggtgttc gagcgccgc cgtcgaccgc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 123

LENGTH: 1044

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 123

atgtctcaga caccgctac aaccgcaaa acgtttccc agatcagctc aagagcgtgg 60
gagcaccgcc cgacccggac cgcccttcc gcgctgcgcc ggctcaaagg ctgcaccag 120
atctgaagc tgatgtggg gatgtgcgg gaacggcagc accggctgct. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 124

LENGTH: 564

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 124

atgactacgc gtcggcaac cgaccgccgc aagatgccca ctgggcggga agaggtagcg 60
gccgcaatcc tgcaggccgc caccgacctg ttcgccgagc gtgggccagc cgcgacgtcg 120
attcgcgaca tcgccgctcg atccaagtc aaccacgggc tgggttttcg. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 125

LENGTH: 702

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 125

gtgacgatat tgatcctgac cgacaacgtc cagcccatg ctctggcggc cgatctgcag 60
gccaggcatg gcgatatgga cgtctatcag tcccccatg gccagctgcc gggtgtcccg 120
cgatgtgatg tcgcagagcg cgtcgcggaa atcgtggagc ggtatgacct. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 126

LENGTH: 1599

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 126

atgttagcct tcccttattt gatgactatg atcaactcac ctaccttga cgttgcgttc 60
atcggcagcg gggccgcgtg ctctatgact ctgctggaaa tggccgatgc cctgctgagc 120
agccctcgg catcgcccaa gttgcgcatc gcggtgggtg agcgagacga. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 127

LENGTH: 1236

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 127

atgaagatcc gaacgttacc cggctcggcg ctggagccgc cgtccgcagt acgcgcgacc 60
ccaggcacgt ccatgttaaa actcgagccg ggtggctcga cgatcccaa gatcccttc 120
atccgccga gtttcccg gccagccgag ctgcccgagg acttcgtaca. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 128

LENGTH: 2358

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 128

atgatcaccg aggacgcctt ccccgtcgaa ccgtggcagg tccgcgagac caagctcaac 60
ctgaacctgc tggcccatc cgaatcccta ttcgcctgt ccaacgggca cattggatta 120
cgcggcaacc tcgacgagg ggaacccttc ggactccgg gcacctacct. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 129

LENGTH: 786

TYPE: DNA

ORGANISM: Mycobacteria ***tuberculosis***

SEQUENCE: 129

atggcgaact ggtatcgccc gaactatccg gaagtgaggt cccgcgtgct gggctctgcc 60
gagaagggtc gtgcttgct gttcgacctc gacggtgtgc tcaccgatac cgcgagcctg 120
cataccaagg cgtggaaggc catgittgac gcctacctag ccgagcgagc. . .

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 130

LENGTH: 60

TYPE: DNA

ORGANISM: M. ***tuberculosis***

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(60)

OTHER INFORMATION: n = A,T,C or G

SEQUENCE: 130

antagtaatg tgcgagctga gcgatgtcgc cgctcccaaa aattaccaat ggttnggtca 60

DETD SEQUENCE CHARACTERISTICS:

SEQ ID NO: 131
 LENGTH: 60
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 131
 agtagtaatg tgcgagctga gcgatgtgc cgcctccaaa aattaccaat ggtttggtca 60
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 133
 LENGTH: 60
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 133
 tgagccttc ctaaccagaa ttgtgaattc atacaagccg tagtcgtgca gaagcgcaac 60
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 134
 LENGTH: 11
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 134
 actcttgag t 11
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 135
 LENGTH: 11
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 135
 actcttgag t 11
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 136
 LENGTH: 49
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(49)
 OTHER INFORMATION: n = A,T,C or G
 SEQUENCE: 136
 gtggcctaca acgngctct ccgnggcgcg ggcgtaccgg atatcttag 49
 DETD SEQUENCE CHARACTERISTICS:
 SEQ ID NO: 137
 LENGTH: 49
 TYPE: DNA
 ORGANISM: M. ***tuberculosis***
 SEQUENCE: 137
 gcggcctaca acggcgctct ccgcggcgcg ggcgtaccgg atatcttag 49
 CLM What is claimed is:
 2. The nucleic acid of claim 1, wherein said nucleic acid hybridizes to
 a M. ***tuberculosis*** complex genome when the deletion is present,
 but not in an undeleted genome.
 4. The nucleic acid of claim 1, wherein said M. ***tuberculosis***
 complex genome is BCG.
 5. The nucleic acid of claim 1, wherein said M. ***tuberculosis***
 complex genome is a variant of M. ***tuberculosis***.
 6. The nucleic acid of claim 1, wherein said M. ***tuberculosis***
 complex genome is M. bovis.
 . . . the nucleic acid of claim 1, and a second nucleic acid that
 hybridizes to a second site in an M. ***tuberculosis*** complex

genome.

14. The genetically altered mycobacterium according to claim 11, wherein said mycobacterium is M. ***tuberculosis***.

16. A method of distinguishing whether a patient has been exposed to BCG or to M. ***tuberculosis***, the method comprising: contacting said patient or a sample derived therefrom with a polypeptide encoded by a deletion marker of Table 1, wherein said deletion marker is present in M. ***tuberculosis*** and absent in BCG; and determining the presence of an immune reaction to said polypeptide, wherein a positive response is indicative of exposure to M. ***tuberculosis***.

19. A method of distinguishing a bacterial strain of the M. ***tuberculosis*** complex, the method comprising: determining the presence of a deletion marker in Table 1, wherein said deletion is absent in. . .

L6 ANSWER 4 OF 8 USPATFULL on STN
AN 2002:294545 USPATFULL
TI DETERMINING THE FUNCTIONS AND INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
IN Eisenberg, David, Los Angeles, CA, UNITED STATES 90024
Rotstein, Sergio, Reading, MA, UNITED STATES 01867
Marcotte, Edward, Los Angeles, CA, UNITED STATES 90064
PA The Regents of the University of California (U.S. corporation)
PI US 2002164588 A1 20021107
AI US 2000-712363 A1 20001113 (9)
RLI Continuation-in-part of Ser. No. WO 2000-US2246, filed on 28 Jan 2000, EXPIRED
PRAI US 1999-60165124 19991112
US 2000-60179531 20000201
US 1999-60165086 19991112
DT Utility
FS APPLICATION
LREP Gregory, Einhorn, Fish & Richardson P.C., 4350 La Jolla Village Drive, San Diego, CA, 92122
CLMN Number of Claims: 33
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 7068
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Abstract of Disclosure

The invention provides novel methods for characterizing the function of nucleic acids and polypeptides. The invention provides a novel method for identifying a nucleic acid or a polypeptide sequence that may be a target for a drug. The invention provides a novel method for identifying a nucleic acid or a polypeptide sequence that may be essential for the growth or viability of an organism. The characterization is based on use of methods of the invention comprising algorithms that can identify functional relationships between diverse sets of non-homologous nucleic acid and polypeptide sequences. The invention provides a computer program product, stored on a computer-readable medium, for identifying a nucleic acid or a polypeptide sequence that may be essential for the growth or viability of an organism. The invention provides a computer program product, stored on a computer-readable medium, for identifying a nucleic acid or a polypeptide sequence that may be a target for a drug. The invention provides a computer system, comprising a processor and a computer program product of the invention.

SUMM . . . nucleic acid or a polypeptide sequence is derived from a pathogen. The pathogen can be a microorganism, such as *Mycobacterium tuberculosis* (MTB).

DETD . . . particularly useful for finding the identifying genes and polypeptides having potential therapeutic relevance in organisms, e.g., microorganisms, such as *Mycobacterium tuberculosis*. The invention also provides *Mycobacterium tuberculosis* genes and polypeptides found by these methods. These genes and polypeptides are useful as potential drug targets.

DETD [0005] The disease *Mycobacterium tuberculosis* (MTB) is one of the world's leading killers. The World Health Organization estimates that 30 million deaths from pulmonary *Mycobacterium tuberculosis* will occur during this decade. Alarming reports on the emergence of drug-resistant strains of this bacterium underscore the importance of . . . new therapeutic agents. Identifying the function of every protein produced by MTB will provide researchers with promising new targets for anti-*Mycobacterium tuberculosis* drug design.

DETD . . . as potential drug targets. One aspect of the invention provides methods for identifying the function of genes and polypeptides from *Mycobacterium tuberculosis* (MTB or TB). Based on this new functional determination, these genes and polypeptides can be used to screen for compositions capable of modifying the physiology and growth of *Mycobacterium tuberculosis* (TB). Thus, genes and polypeptides identified by the methods of the invention, including the genes and polypeptides identified herein, can . . .

DETD . . . potential drug targets; see Figure 1, which shows an analysis of InhA, the target for isoniazid, the most widely used anti-*Mycobacterium tuberculosis* drug, and functional linkages to a set of genes mostly known or hypothesized to be involved in cell wall-related processes. . .

DETD . . . top-scoring polypeptides with high similarity (BLAST alignment E-value < 10⁻²⁰) to polypeptides identified in a known pathway. For example, *Mycobacterium tuberculosis* proteins were so analyzed against *E. coli* proteins; MTB proteins whose *E. coli* homologs (i.e., having high similarity by BLAST) . . . identified by other techniques, such as traditional sequence homology or sequence identity comparison techniques. Several known drug targets in *Mycobacterium tuberculosis* were used with the methods of the invention to use functional linkages to identify potential new drug targets in the same pathways as the known drug targets. There are very few drugs that are effective for anti-*Mycobacterium tuberculosis* therapy, since the complex lipid-rich mycobacterial cell wall is impermeable to many antibacterial agents. Additionally, single- and multi-drug resistance is rapidly emerging against these drugs. To address this issue, the methods of the invention were used to identify *Mycobacterium tuberculosis* (MTB or TB) proteins that are functionally linked to the targets of known drugs. Inhibiting these proteins should have the . . . the functional linkages of the known drug targets was examined. Isoniazid. This is one of the most widely used of all anti-*Mycobacterium tuberculosis* drugs. It is believed that the compound is activated by the catalase-peroxidase KatG. Once activated, it then attaches to a . . . Rozwarski (1998) Science 279:98-102. Using the "phylogenetic profile, the inhA gene was "linked," or functionally associated with, to two polyketide synthases, *pks1* and *pks6* (Figure 1), both of which contain acyl carrier protein motifs. The polyketide synthase *pks6* is in turn known. . . various tRNA synthases and ribosomal proteins. However, no functional links to uncharacterized proteins were found. Ethambutol. This drug is effective against *Mycobacterium tuberculosis* when used in combination with isoniazid. It is believed that the drug interacts with the EmbB protein, a probable arabinosyl-transferase, . . . uncharacterized genes by the

"phylogenetic profile" method; see Figure 2, which shows an analysis of EmbB, the target for the anti- ***tuberculosis*** drug Ethambutol, and shows functional linkages to genes mostly of unknown function but with some indications of localization at the . . . the "domain fusion" method, the "phylogenetic profile" method or the "physiologic linkage" method, or a combination thereof, as described herein. Approximately eleven M. ***tuberculosis*** proteins are indicated by sequence homology to be penicillin-binding proteins, thought to synthesize peptidoglycan in the course of cell elongation. . . and given the importance of htrA in S. typhimurium pathogenesis, this pathway represents another potential source of novel targets for anti- ***tuberculosis*** drugs. Proteins linked to essential proteins The invention also provides a novel method for identifying a polypeptide, or the nucleic acid sequence. . .

DETD . . . list of 734 genes that are essential for Saccharomyces cerevisiae viability (see, e.g., Mewes (1999) supra). A list of Mycobacterium ***tuberculosis*** genes orthologous to these essential genes was generated. Using the methods of the invention, 60 such genes were found. The products of these genes have a high likelihood of also being essential to the ***tuberculosis*** bacterium and therefore could be promising therapeutic targets. Furthermore, since the list of essential genes came from a eukaryote, there. . . an organism for which essential genes are known is calculated. For example, as discussed herein, the query genome is Mycobacterium ***tuberculosis*** (TB) and the genome with known essentials is the yeast S. cerevisiae. Sequence homology between all TB genes and all. . . filtering step are the predicted drug targets for the query organism. As a benchmark, this method was applied to the M. ***tuberculosis*** genome. Of the over 3900 genes in TB, 11 were identified as potential drug targets. Comparing this list of 11. . . effectiveness of this method to identify novel drug targets was clearly demonstrated when the algorithm was applied to the M. ***tuberculosis*** genome. The specific inhibition of the MTB homologs might be difficult. To address this issue, using the methods of the invention, . . .

DETD [0111] > ***Rv0405*** pks6 TB.seq 485729:489934 MW:147615
 >emb|AL123456|MTBH37RV:485729-489937, pks6 SEQ ID
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 TAGCGATTCCCGGCGACCTCGGTGACAGATTTGGGTTTGTATTCCCGATTGGCCGTTTGGGATAATCCTA
 GCGCTAATGATTGATTGATAGTCTGTTGAACGAGCGTAGTGCTGACTCGTTAAGAGAGAGTTCATGGACACG
 CCGACAGGAACACGCAGGGTTCGGGGCAGCATAAACGAGCCGGTTGCGGTTCATCGGAGTGGGCTGTGATTTT
 CGGGAGATATTGACGGCCCGGAACGGCTATGGGACTTTCTGACCGAGAAGAAGTGTGCGATAACAGCGTATC
 CAGATCGTGGGTTACGAATGCTGGAACCTTCGCGGAGTCCGGAGGCTTTTTAAAGGATGTCGCGGGTTTCG
 ATAATAGATTTTTTATATCCCGCCGGACGAGGCTCTGCGAATGGATCCGCAACAACGGTTGTTACTGGAGG
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 GCGATATCGCACTTGTCGGTGGGACGAATGTTCTTATTTACACAGAACCATGGGGTGGGTTTAGGGAAGCGG
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 GTTCAGCGGTCAATCAGGACGGTAAGTCCAACGGTATTATGGCGCCAAATCCTAGTGCGCAAAATGGTGTTT
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CAAACCCGGCGGAGCGAATCGATGCGCTCACCGATCTTTTCTACAAGCTTGCATGCGGGTCGGGATGCCG
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CGAAGAACGTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTCTAACTGTGC
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DETD [0206] > ***Rv2946c*** ***pksI*** TB.seq 3291503:3296350

MW:166642 >emb|AL123456|MTBH37RV:c3296350-3291500, ***pksI*** SEQ
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DETD [0257] > ***Rv0405*** pks6 TB.seq 485729:489934 MW:147615 SEQ ID

NO:166MTDGSVTADKLQKWFREYLSHIEHPNEVSLDVPIRDGLKSIDVLAIPGDLGDRFGFCIPDLAV
WDNPSANDLIDSLNQRSADSLRESHGHADRNTQGRGSINEPVAVIGVGRFPGDIDGPERLWDFLTEKKCA
ITAYPDRGFTNAGTFAESGGFLKDVAGFDNRFFDIPDEALRMDPQQRLLLEVSWEALEHAGIIPESLRLSR
TGVFVGVSSDYVRLVSASAQKSTIWDNTGGSSIIANRISYFLDIQGPSIVIDTACSSSLVAVHLACRSL
STWDCDIALVGGTNVLISPEPWGGFREAGILSQTGCCHAFDKSADGMVRGEGCGVIVLQRLSDARLEGRIL
AILTGSAVNQDGKSNIGMAPNPSAQIGVLENACKSARVDPLEIGYVEAHGTGTSLGDRIEAHALGMVFGRKR
PGSGPLMIGSIKPNIGHLEGAAGIAGLIKAVLMVERGSLLPSGGFTFPNPAIPFTELGLRVVDELQEWPVVA
GRPRRAGVSSFGFGGTNAHVIVVEAGSVGADTVSGRADVGGSGGGVVAWVISGKTASALAAQAGRLGRYVRA
RPALDVVDVGYSLVSTRSVFDHRAVVVGQTRDELLAGLAGVAVAGRPEAGVVCVGKPAKTAFFVAGQGSQW
LGMGSELYAAYPVFAEALDAVVDELDRHLRYPLRDVIWGHQDQLLNTTEFAQPALFAVEVALYRLLMSWGV
PGLVLGHSVGEALAAHVAGALCLPDAAMLVAARGRLMQALPAGGAMFAVQAREDEVAPMLGHDVSIAAVNGP
ASVVGHAHDVSAIADRLRGQRRVRHLAVSHAFHSALMEPMIAEFTAVAAELSVGLTPTIPVISNVTGQLV
ADDFAADYWARHIRAVVRFGDSVRSACASRFIEVPGGGTSLIEASLADAQIVSVPTLRKDRPEPVS
VMTAAQGFVSGMGLDWASVFSGYRPKRVELPTYAFQHQKFWLAPAPSVSDPTAAGQIGASDGGAEGLASSG
FAARLAGRSADQLAAAEVCEHAAAVLGRDGAAGLDAGQAFADSGFNSLSAVELRNRLTAVTAVTLPAT
IFDHPTTELAQYLITQIDGHGSSAAAAANPAERIDALTDLFLQACDAGRDADGWKMVALASNTRERMSSPV

RNNVSKNVALLADGISDVVICIPTLTVLSDQREYRDIANAMTGRHSVYSLTLPFGDSSDALPQNADMIVET
VSNAIIDVVGSCRFVLSGYSSGGVLAYALCSHLSVKHQRNPLGVALIDTYLPSQIANPSMNEGFSPNDTGK
GLSREVIRVARMLNRLTATRLTAAATYAAIFQAWEPGRSMAPVLNIVAKDRIATVENLREERINRWRTAAAE
AAYSVAEVPGDHFGMMSTSSSEAIATEIHDWISGLVRGPHR

DETD [0353] > ***Rv2946c*** ***pks1*** TB.seq 3291503:3296350

MW:166642 SEQ ID NO:262VISARSAEALTAQAGRLMAHVQANPGLDPIDVGCSLASRSVFEHRAV
VVGASREQLIAGLAGLAAGEPGAGVAVGQPGSVGKTVVVFPGQGAQRIGMGRELYGELPVFAQAFDAVADEL
DRHLRLPLRDVIWGADADLLDSTEFAPALFAVEVASFAVLRDWGVLPDFVMGHSVGEIAAAHAAGVLTAD
AAMLVVARGRLMQALPAGGAMVAVAASEDEVEPLLGEVGIAAINAPESVVISGAQAAANAIADRFQAAQGR
VHQLAVSHAFHSPLMEPMLEEFARVAARVQAREPQLGLVSNVTGELAGPDFGSAQYWVDHVRPVRFAFSAR
HLQTLGATHFIEAGPGSGLTGSIEQLAPAEAMVVSMLGKDRPELASALGAAGQVFTTGVPVQWSAVFAGSG
GRRVQLPTYAFQRRRFWETPGADGPADAAGLGLGATEHALLGAVVERPDSDEVVLTGRLSLADQPWLADHV
NGVVLFPAGFVELVIRAGDEVGCALIEELVLAAPLVMHPGVGVQVQVVVGAADESGHRAVSVSRRGDSQSG
WLLNAEGLMGVAAAETPMDLSVWPPEGAESVDISDGYAQLAERGYAYGPAFQGLVAIWRRGSELF AEV VAPG
EAGVAVDRMGMPHAPVLDVAVLHALGLAVEKTQASTETRLPFCWRGVSLHAGGAGRVARFASAGADAISVDVC
DATGLPVLTVRSLVTRPITAEQLRAAVTAAGGASDQGPLEVWSPISVVS GGANGSAPPAPVSWADFCAGSD
GDASVVVWELESAGGQASSVVGSVYAATHTALEVLQSWLGADRAATLVVLT HGGVGLAGEDISDLAAA VWG
MARSAQAENPGRIVLIDTDAAVDASVLAVGEPQLLVGGTVHAPRLSPAPALLALPAESA WRLAAGGGGT
LEDLVIQPCPEVQAPLQAGQVRVAVAAVGVNFRDVVAALGMYPGQAPPLGAEGAGVVLETGPEVTDLAVGDA
VMGFLGGAGPLAVVDQQLVTRVPQGW SFAQAAAVPVFLTA WYGLADLAEIKAGESVLIHAGTGGVGMAAVQ
LARQWGVVEFVTASRGKWDTLRAMGFDDDHIGDSRTCEFEKFLAVTEGRGVDVVLDSLAGEFVDASLRLLV
RGGRFLEMGKTDIRDAQEIAANYPGVQYRAFDLSEAGPARMQEMLAEVRELFDRELHRLPVTTWVRCAPA
AFRFMSQARHIGKVVLTPMSALADRLADGTVVITGATGAVGGVRLARHLVGAYGVRHLVLSRRGDRAEGAAE
LAADLTEAGAKVQVVACDVADRAAVAGLFAQLSREYPPVRGVIHAAGVLD DAVITSLTPDRIDTVLRAKVDA
AWNHLQATSDLDLSMFALCSSIAATVSGPGQGNYSANAFDGLAAHRQAAGLAGISLAWGLWEQPGGMTAH
LSSRDLARMSRGLAPMSPAEAVELFDAALIDHPLAVATLLDRAALDARAQAGALPALFSGLARRPRRRQI
DDTGDATSSKSALAQRHLHGLAADEQLELLVGLVCLQAAAVLGRPSAEDVDPDTEFGDLGFDSLTAVELNRNL
KTATGLTLPTVIFDHPTPTAVAEYVAQMQSGSRPTESGDPTSQVVEPAAAEVSVHA

CLM What is claimed is:

6.The method of claim 1 or claim 2, wherein the microorganism is
Mycobacterium ***tuberculosis*** (MTB).

L6 ANSWER 5 OF 8 LIFESCI COPYRIGHT 2003 CSA on STN

AN 2002:111087 LIFESCI

TI Role of the pks15/1 Gene in the Biosynthesis of Phenolglycolipids in the
Mycobacterium ***tuberculosis*** Complex. Evidence that all strains
synthesize glycosylated p-hydroxybenzoic methyl esters and that strains
devoid of phenolglycolipids harbor a frameshift mutation in the pks15/1
gene

AU Constant, P.; Perez, E.; Malaga, W.; Laneelle, M.; Saurel, O.; Daffe, M.;
Guilhot, C.

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SO Journal of Biological Chemistry [J. Biol. Chem.], (20021011) vol. 277, no.
41, pp. 38148-38158.
ISSN: 0021-9258.

DT Journal

FS G; J

LA English

SL English

AB Diesters of phthiocerol and phenolphthiocerol are important virulence
factors of Mycobacterium ***tuberculosis*** and Mycobacterium leprae,
the two main mycobacterial pathogens in humans. They are both long-chain
[beta]-diols, and their biosynthetic pathway is beginning to be
elucidated. Although the two classes of molecules share a common lipid
core, phthiocerol diesters have been found in all the strains of the M.
tuberculosis complex examined although phenolphthiocerol diesters
are produced by only a few groups of strains. To address the question of

the origin of this diversity 8 reference strains and 10 clinical isolates of *M. tuberculosis* were analyzed. We report the presence of glycosylated p-hydroxybenzoic acid methyl esters, structurally related to the type-specific phenolphthiocerol glycolipids, in the culture media of all reference strains of *M. tuberculosis*, suggesting that the strains devoid of phenolphthiocerol derivatives are unable to elongate the putative p-hydroxybenzoic acid precursor. We also show that all the strains of *M. tuberculosis* examined and deficient in the production of phenolphthiocerol derivatives are natural mutants with a frameshift mutation in *pksl5/1* whereas a single open reading frame for *pksl5/1* is found in *Mycobacterium bovis* BCG, *M. leprae*, and strains of *M. tuberculosis* that produce phenolphthiocerol derivatives.

Complementation of the H37Rv strain of *M. tuberculosis*, which is devoid of phenolphthiocerol derivatives, with the fused *pksl5/1* gene from *M. bovis* BCG restored phenolphthiocerol glycolipids production.

Conversely, disruption of the *pksl5/1* gene in *M. bovis* BCG led to the abolition of the synthesis of type-specific phenolphthiocerol glycolipid. These data indicate that *Pks15/1* is involved in the elongation of p-hydroxybenzoic acid to give p-hydroxyphenylalkanoates, which in turn are converted, presumably by the *PpsA-E* synthase, to phenolphthiocerol derivatives.

TI Role of the *pksl5/1* Gene in the Biosynthesis of Phenoglycolipids in the *Mycobacterium tuberculosis* Complex. Evidence that all strains synthesize glycosylated p-hydroxybenzoic methyl esters and that strains devoid of phenoglycolipids harbor a frameshift mutation. . .

AB Diesters of phthiocerol and phenolphthiocerol are important virulence factors of *Mycobacterium tuberculosis* and *Mycobacterium leprae*, the two main mycobacterial pathogens in humans. They are both long-chain [beta]-diols, and their biosynthetic pathway is. . . classes of molecules share a common lipid core, phthiocerol diesters have been found in all the strains of the *M. tuberculosis* complex examined although phenolphthiocerol diesters are produced by only a few groups of strains. To address the question of the origin of this diversity 8 reference strains and 10 clinical isolates of *M. tuberculosis* were analyzed. We report the presence of glycosylated p-hydroxybenzoic acid methyl esters, structurally related to the type-specific phenolphthiocerol glycolipids, in the culture media of all reference strains of *M. tuberculosis*, suggesting that the strains devoid of phenolphthiocerol derivatives are unable to elongate the putative p-hydroxybenzoic acid precursor. We also show that all the strains of *M. tuberculosis* examined and deficient in the production of phenolphthiocerol derivatives are natural mutants with a frameshift mutation in *pksl5/1* whereas a single open reading frame for *pksl5/1* is found in *Mycobacterium bovis* BCG, *M. leprae*, and strains of *M. tuberculosis* that produce phenolphthiocerol derivatives.

Complementation of the H37Rv strain of *M. tuberculosis*, which is devoid of phenolphthiocerol derivatives, with the fused *pksl5/1* gene from *M. bovis* BCG restored phenolphthiocerol glycolipids production. Conversely. . .

UT Lipids; phthiocerol; phenolphthiocerol; *pksl5* gene; *pksl* gene; Glycolipids; *Mycobacterium tuberculosis*; *Mycobacterium bovis*; *Mycobacterium leprae*

L6 ANSWER 6 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 1

AN 2002:526838 BIOSIS

DN PREV200200526838

TI Definition of the first mannosylation step in phosphatidylinositol mannoside synthesis. *PimA* is essential for growth of mycobacteria.

AU Kordulakova, Jana; Gilleron, Martine; Mikusova, Katarina; Puzo, Germain; Brennan, Patrick J.; Gicquel, Brigitte; Jackson, Mary (1)

CS (1) Unite de Genetique Mycobacterienne, Institut Pasteur, 25 Rue du Dr.
Roux, 75724, Paris Cedex 15: mjackson@pasteur.fr France
SO Journal of Biological Chemistry, (August 30, 2002) Vol. 277, No. 35, pp.
31335-31344. <http://www.jbc.org/>. print.
ISSN: 0021-9258.

DT Article

LA English

AB We examined the function of the pimA (***Rv2610c***) gene, located in the vicinity of the phosphatidylinositol synthase gene in the genomes of Mycobacterium ***tuberculosis*** and Mycobacterium smegmatis, which encodes a putative mannosyltransferase involved in the early steps of phosphatidylinositol mannoside synthesis. A cell-free assay was developed in which membranes from M. smegmatis overexpressing the pimA gene incorporate mannose from GDP-(14C)Man into di- and tri-acylated phosphatidylinositol mono-mannosides. Moreover, crude extracts from Escherichia coli producing a recombinant PimA protein synthesized diacylated phosphatidylinositol mono-mannoside from GDP-(14C)Man and bovine phosphatidylinositol. To determine whether PimA is an essential enzyme of mycobacteria, we constructed a pimA conditional mutant of M. smegmatis. The ability of this mutant to synthesize the PimA mannosyltransferase was dependent on the presence of a functional copy of the pimA gene carried on a temperature-sensitive rescue plasmid. We demonstrate here that the pimA mutant is unable to grow at the higher temperature at which the rescue plasmid is lost. Thus, the synthesis of phosphatidylinositol mono-mannosides and derived higher phosphatidylinositol mannosides in M. smegmatis appears to be dependent on PimA and essential for growth. This work provides the first direct evidence of the essentiality of phosphatidylinositol mannosides for the growth of mycobacteria.

AB We examined the function of the pimA (***Rv2610c***) gene, located in the vicinity of the phosphatidylinositol synthase gene in the genomes of Mycobacterium ***tuberculosis*** and Mycobacterium smegmatis, which encodes a putative mannosyltransferase involved in the early steps of phosphatidylinositol mannoside synthesis. A cell-free assay. . .

ORGN . . .

Microorganisms; Mycobacteriaceae: Mycobacteria, Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms

ORGN Organism Name

Escherichia coli (Enterobacteriaceae); Mycobacterium smegmatis (Mycobacteriaceae); Mycobacterium ***tuberculosis*** (Mycobacteriaceae)

ORGN Organism Superterms

Bacteria; Eubacteria; Microorganisms

L6 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN

AN 2001:208420 CAPLUS

DN 134:247979

TI Virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines

IN Trucksis, Michele

PA University of Maryland, Baltimore, USA; United States Government, as Represented by Department of Veterans Affairs

SO PCT Int. Appl., 99 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 2001019993	A2	20010322	WO 2000-US25512	20000918
WO 2001019993	A3	20011122		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-154322P P 19990917

AB Methods for identifying, isolating and mutagenizing virulence genes of mycobacteria, e.g., *Mycobacterium marinum* and *M. tuberculosis*, are described. The *M. marinum* signature-tagged mutant library was generated and screened for mutants which exhibit a reduced ability to survive in the goldfish model. Wild type *M. marinum* virulence genes which correspond to the genes disrupted by transposon in avirulent mutants were isolated. *M. tuberculosis* genes homologous to *M. marinum* virulence genes were isolated and characterized. Also described are isolated virulence genes and fragments of them, isolated gene products and fragments of them, avirulent bacteria in which one or more virulence genes are mutagenized, attenuated vaccines contg. such mutant bacteria, and methods to elicit an immune response in a host, using such mutant bacteria.

TI Virulence genes of *Mycobacterium marinum* and *M. tuberculosis*, avirulent mutant mycobacteria and attenuated vaccines

AB Methods for identifying, isolating and mutagenizing virulence genes of mycobacteria, e.g., *Mycobacterium marinum* and *M. tuberculosis*, are described. The *M. marinum* signature-tagged mutant library was generated and screened for mutants which exhibit a reduced ability to survive in the goldfish model. Wild type *M. marinum* virulence genes which correspond to the genes disrupted by transposon in avirulent mutants were isolated. *M. tuberculosis* genes homologous to *M. marinum* virulence genes were isolated and characterized. Also described are isolated virulence genes and fragments of them, isolated gene products and fragments of them, avirulent bacteria in which one or more virulence genes are mutagenized, attenuated vaccines contg. such mutant bacteria, and methods to elicit an immune response in a host, using such mutant bacteria.

IT Gene, microbial

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (008381, of *M. tuberculosis*; virulence genes of *Mycobacterium marinum* and *M. tuberculosis*, avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (CY20G9.23, of *M. tuberculosis*; virulence genes of *Mycobacterium marinum* and *M. tuberculosis*, avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (Rv0236c, of *M. tuberculosis*; virulence genes of *Mycobacterium marinum* and *M. tuberculosis*, avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP

(Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***Rv0822c*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***Rv0987*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***Rv1954c*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***Rv2181*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (Rv2348, of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***Rv2610c*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***Rv3137*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***Rv3268*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (Rv3511, of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)

- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (Rv3775, of M. *****tuberculosis***** ; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (Rv3860, of M. *****tuberculosis***** ; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT *Mycobacterium marinum*
Mycobacterium *****tuberculosis*****
 (avirulent mutant; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Vaccines
 (contg. mutant mycobacteria; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (mbtB, of M. *****tuberculosis***** ; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (mbtE, of M. *****tuberculosis***** ; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Goldfish (*Carassius auratus*)
 (mutant M. marinum-infected model; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (npr (pirE), of M. *****tuberculosis***** ; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Drug delivery systems
 (of attenuated vaccine; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Protein sequences
 (of virulence gene-encoded proteins of M. marinum and M. *****tuberculosis***** ; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)
- IT DNA sequences
 (of virulence genes of M. marinum and M. *****tuberculosis***** ; virulence genes of *Mycobacterium marinum* and M. *****tuberculosis***** , avirulent mutant mycobacteria and attenuated vaccines)

- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (pks002c, of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***pks1*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (pks6, of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (pks8, of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (***pks9*** , of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (ppsE, of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Mutation
 (rendering reduced virulence; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Transposons
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (signature-tagged, mutagenesis using; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (smc, of M. ***tuberculosis*** ; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Mutagenesis
 (transposon; virulence genes of Mycobacterium marinum and M.

- ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Polyketides
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
 (using polyketide synthase gene; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Fish
 (vaccination against M. marinum infection; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Immunization
 (vaccination; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Molecular cloning
 Mycobacterium
 Virulence (microbial)
 (virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Primers (nucleic acid)
 Probes (nucleic acid)
 RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Gene, microbial
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (virulence, screening for, disruption of; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT Proteins, specific or class
 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (virulence-assocd.; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT 331010-57-2 331010-58-3 331010-59-4 331010-60-7 331010-61-8
 331010-62-9 331010-63-0 331010-64-1 331010-66-3 331010-70-9
 331249-85-5 331249-86-6 331249-87-7 331249-88-8 331257-62-6
 331257-63-7 331257-69-3 331257-85-3 331257-86-4 331257-87-5
 331257-88-6 331257-89-7 331257-90-0
 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (amino acid sequence; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT 79956-01-7P, Polyketide synthase
 RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); CAT (Catalyst use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (gene ppsE, pks6, ***pks9*** , ***pks1*** or pks002c; virulence genes of Mycobacterium marinum and M. ***tuberculosis*** , avirulent mutant mycobacteria and attenuated vaccines)
- IT 330416-91-6 330416-92-7 330416-93-8 330416-94-9 330416-95-0
 330416-96-1 330416-97-2 330416-99-4 330417-00-0 330417-02-2
 330417-04-4 330417-06-6 331010-65-2 331010-67-4 331010-68-5
 331010-69-6 331010-71-0
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP

(Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; virulence genes of Mycobacterium marinum and M. ***tuberculosis***, avirulent mutant mycobacteria and attenuated vaccines)

IT 180065-72-9 180065-74-1 195283-77-3, 3: PN: WO0119993 SEQID: 3
unclaimed DNA 331011-42-8

RL: PRP (Properties)
(unclaimed nucleotide sequence; virulence genes of Mycobacterium marinum and M. ***tuberculosis***, avirulent mutant mycobacteria and attenuated vaccines)

IT 331011-43-9

RL: PRP (Properties)
(unclaimed sequence; virulence genes of Mycobacterium marinum and M. ***tuberculosis***, avirulent mutant mycobacteria and attenuated vaccines)

L6 ANSWER 8 OF 8 USPATFULL on STN

AN 2001:158022 USPATFULL

TI Molecular differences between species of the M. ***tuberculosis*** complex

IN Behr, Marcel, Montreal, Canada

Small, Peter, Stanford, CA, United States

Schoolnik, Gary, Stanford, CA, United States

Wilson, Michael A., Stanford, CA, United States

PA The Board of Trustees of the Leland Stanford Junior University, Palo Alto, CA, United States (U.S. corporation)

PI US 6291190 B1 20010918

AI US 1999-318191 19990525 (9)

PRAI US 1998-97936P 19980825 (60)

DT Utility

FS GRANTED

EXNAM Primary Examiner: Guzo, David; Assistant Examiner: Leffers, Jr., Gerald G.

LREP Sherwood, Pamela J.Bozicevic, Field & Francis LLP

CLMN Number of Claims: 5

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 1377

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Specific genetic deletions are identified in mycobacteria isolates, including variations in the M. ***tuberculosis*** genome sequence between isolates, and numerous deletion present in BCG as compared to M. tb. These deletions are used as markers to distinguish between pathogenic and avirulent strains, and as a marker for particular M. tb isolates. Deletions specific to vaccine strains of BCG are useful in determining whether a positive tuberculin skin test is indicative of actual ***tuberculosis*** infection. The deleted sequences may be re-introduced into BCG to improve the efficacy of vaccination. Alternatively, the genetic sequence that corresponds to the deletion(s) are deleted from M. bovis or M. ***tuberculosis*** to attenuate the pathogenic bacteria.

TI Molecular differences between species of the M. ***tuberculosis*** complex

AB Specific genetic deletions are identified in mycobacteria isolates, including variations in the M. ***tuberculosis*** genome sequence between isolates, and numerous deletion present in BCG as compared to M. tb. These deletions are used as . . . specific to vaccine strains of BCG are useful in determining whether a positive tuberculin skin test is indicative of actual ***tuberculosis*** infection. The deleted sequences may be re-introduced into BCG to improve the efficacy of

vaccination. Alternatively, the genetic sequence that corresponds to the deletion(s) are deleted from M. bovis or M. ***tuberculosis*** to attenuate the pathogenic bacteria.

SUMM ***Tuberculosis*** is an ancient human scourge that continues to be an important public health problem worldwide. It is an ongoing epidemic of staggering proportions. Approximately one in every three people in the world is infected with Mycobacterium ***tuberculosis***, and has a 10% lifetime risk of progressing from infection to clinical disease. Although ***tuberculosis*** can be treated, an estimated 2.9 million people died from the disease last year.

SUMM There are significant problems with a reliance on drug treatment to control active M. ***tuberculosis*** infections. Most of the regions having high infection rates are less developed countries, which suffer from a lack of easily accessible health services, diagnostic facilities and suitable antibiotics against M. ***tuberculosis***. Even where these are available, patient compliance is often poor because of the lengthy regimen required for complete treatment, and. . .

SUMM Prevention of infection would circumvent the problems of treatment, and so vaccination against ***tuberculosis*** is widely performed in endemic regions. Around 100 million people a year are vaccinated with live bacillus Calmette-Guerin (BCG) vaccine. . . Unfortunately, the vaccine is widely variable in its efficacy, providing anywhere from 0 to 80% protection against infection with M. ***tuberculosis***.

SUMM BCG has an interesting history. It is an attenuated strain of M. bovis, a very close relative of M. ***tuberculosis***. The M. bovis strain that became BCG was isolated from a cow in the late 1800's by a bacteriologist named. . .

SUMM . . . as health care professionals likely to be exposed to tubercle bacilli. Recombinant DNA vaccines bearing protective genes from virulent M. ***tuberculosis*** are being developed using shuttle plasmids to transfer genetic material from one mycobacterial species to another, for example see U.S. Pat. No. 5,776,465. ***Tuberculosis*** vaccine development should be given a high priority in current medical research goals.

SUMM . . . and virulent M. bovis. Subtractive genomic hybridization was used to identify genetic differences between virulent M. bovis and M. ***tuberculosis*** and avirulent BCG. U.S. Pat. No. 5,700,683 is directed to these genetic differences.

SUMM Cole et al. (1998) Nature 393:537-544 have described the complete genome of M. ***tuberculosis***. To obtain the contiguous genome sequence, a combined approach was used that involved the systematic sequence analysis of selected large-insert. . .

SUMM Mycobacterium ***tuberculosis*** (M.tb.) genomic sequence is available at several internet sites.

SUMM Genetic markers are provided that distinguish between strains of the Mycobacterium ***tuberculosis*** complex, particularly between avirulent and virulent strains. Strains of interest include M. bovis, M. bovis BCG strains, M. ***tuberculosis*** (M. tb.) isolates, and bacteriophages that infect mycobacteria. The genetic markers are used for assays, e.g. immunoassays, that distinguish between. . .

SUMM . . . that serve as markers to distinguish between avirulent and virulent mycobacteria strains, including M. bovis, M. bovis BCG strains, M. ***tuberculosis*** (M. tb.) isolates, and bacteriophages that infect mycobacteria. These deletions are used as genetic markers to distinguish between the. . .

SUMM Identification of M. ***Tuberculosis*** Complex Deletion Markers

SUMM . . . Rv2346c MTCY98.15c "H37Rv, segment

NO: 54 103: 17622, 26584"

SEQ ID RD07 Rv2347c MTCY98.16c "H37Rv, segment

NO: 55 103: 17622, 26584"

SEQ ID RD07 ***Rv2348c*** MTCY98.17c "H37Rv, segment

NO: 56 103: 17622, 26584"
SEQ ID RD07 Rv2349c MTCY98.18c "H37Rv, segment
NO: 57 103: 17622, 26584"

SEQ ID RD07 Rv2350c. . .
SUMM . . . American Type Culture Collection, Rockville, Md, USA;

SSI = Statens Serum Institute, Copenhagen, Denmark;

CL = Connaught Laboratories, Willowdale, Canada,

JATA = Japanese Anti- ***Tuberculosis*** Association;

INH = isoniazid.

Canadian: BCG's refers to BCG-Montreal and BCG-Toronto, the latter being derived from the former.

SUMM . . . of the fluorochrome tagged nucleotides used to label the selected probe. The strains used were the reference strain of *Mycobacterium* ***tuberculosis*** (H37Rv), other *M. tb.* laboratory strains, such as H37Ra, the O strain, *M. tb.* clinical isolates, the reference strain of. . .

SUMM As used herein, the term "deletion marker", or "marker" is used to refer to those sequences of *M. ***tuberculosis**** complex genomes that are deleted in one or more of the strains or species, as indicated in Table 1. The bacteria of the *M. ***tuberculosis**** complex include *M. ***tuberculosis****, *M. bovis*, and BCG, inclusive of varied isolates and strains within each species. Nucleic acids of interest include all or. . .

SUMM . . . genomic sequence. For example, the deletion found in *M. bovis*, at Rv0221, corresponds to the nucleotide sequence of the *M. ***tuberculosis**** H37Rv genome, segment 12: 17432,19335. The junction comprises the regions upstream of position 17342, and downstream of 19335, e.g. a. . .

SUMM . . . of the provided deletion markers. Arrays of interest may further comprise other genetic sequences, particularly other sequences of interest for ***tuberculosis*** screening. The oligonucleotide sequence on the array will usually be at least about 12 nt in length, may be the. . .

SUMM . . . particular infection or isolate is pathogenic. The term mycobacteria may refer to any member of the family *Mycobacteriaceae*, including *M. ***tuberculosis****, *M. avium* complex, *M. kansasii*, *M. scrofulaceum*, *M. bovis* and *M. leprae*.

SUMM *Mycobacterium*, particularly those of the *M. ***tuberculosis**** complex, are genetically engineered to contain specific deletions or insertions corresponding to the identified genetic markers. In particular, attenuated BCG. . . are modified to introduce deleted genes encoding sequences important in the establishment of effective immunity. Alternatively, *M. bovis* or *M. ***tuberculosis**** are modified by homologous recombination to create specific deletions in sequences that determine virulence, i.e. the bacteria are attenuated through. . .

SUMM . . . an alternative embodiment, one or more of the deletions provided in Table 1 are introduced into a strain of *M. ***tuberculosis**** or *M. bovis*. Preferably such a strain is reduced in virulence, e.g. H37Ra, etc. Methods of homologous recombination in. . .

SUMM . . . assay, mammalian macrophages, preferably human macrophages, are infected. In a comparison of virulent, avirulent and attenuated strains of the *M. ***tuberculosis**** complex, alveolar or peripheral blood monocytes are infected at a 1:1 ratio (Silver et al. (1998) *Infect Immun* 66(3):1190-1199; Paul. . .

SUMM . . . *tb.* complex bacteria are able to infect a wide variety of animal hosts. One model of particular interest is cavitory ***tuberculosis*** produced in rabbits by aerosolized virulent tubercle bacilli (Converse et al. (1996) *Infect Immun* 64(11):4776-4787). In liquefied caseum, the tubercle. . . and also to other people. Of

the commonly used laboratory animals, the rabbit is the only one in which cavitary ***tuberculosis*** can be readily produced.

SUMM . . . known in the art. Vaccines of the modified bacteria are administered to a host which may be exposed to virulent ***tuberculosis***. In many countries where ***tuberculosis*** is endemic, vaccination may be performed at birth, with additional vaccinations as necessary. The compounds of the present invention are.

DETD Therefore, with the preparation for an array that contained the whole genome of Mycobacterium ***tuberculosis***, we compared BCG-Connaught to Mycobacterium ***tuberculosis***, using the array for competitive hybridization. The protocol follows:

DETD . . . different fluorescent dyes, it is possible to determine that a spot of DNA on the array has hybridized to Mycobacterium ***tuberculosis*** (green dye) and not to BCG (red dye), thus demonstrating a likely deletion from the BCG genome.

DETD . . . probing for different DNA sequences. For the purposes of this project, we include DNA from the reference strain of Mycobacterium ***tuberculosis*** (H37Rv), from other laboratory strains, such as H37Ra, the O strain, from clinical isolates, from the reference strain of Mycobacterium. . .

DETD . . . of the genome database is performed to determine whether the sequence is exactly identical to one part of the Mycobacterium ***tuberculosis*** genome, and that the next part of the amplicon is exactly identical to another part of the Mycobacterium ***tuberculosis*** genome. This permits precise identification of the site of deletion.

DETD emb .vertline.Z79701 .vertline.MTCY277 Mycobacterium ***tuberculosis*** cosmid Y277

Length = 38,908

Plus Strand HSPs:

Score = 643 (177.7 bits), Expect = 1.6e-54, Sum P(2) = 1.6e-54

Identities = 129/131 (98%),. . .

CLM What is claimed is:

1. A method of distinguishing whether a patient has been exposed to a virulent strain of the M. ***tuberculosis*** complex, the method comprising: contacting said patient or a sample obtained therefrom with a polypeptide encoded by the open reading. . . immune reaction to said polypeptide, wherein a positive response is indicative of exposure to a virulent strain of the M. ***tuberculosis*** complex.